

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:52:49 ; Search time 1953 Seconds

(without alignments)  
16460.851 Million cell updates/sec

Title: US-09-884-2lla-2

Perfect score: 1985

Sequence: 1 ctaagaccgtggggaggcag.....gaaataaaaaaaaaaaaaa 1985

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estnu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

20: em\_gss\_pln.\*

21: em\_gss\_vrt.\*

22: em\_gss\_fun.\*

23: em\_gss\_mam.\*

24: em\_gss\_mus.\*

25: em\_gss\_other.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
c 1	421.2	21.2	877	17	CNS02HJ0
c 2	397.2	20.0	905	17	CNS02KZT
c 3	297.4	15.0	1185	17	CNS02W1W
5	252	12.7	501	17	CNS03X7L
5	242.6	12.2	521	12	BF192805
c 6	234	11.8	1017	13	BI830442
					BI830442 603073302

7	222.6	11.2	1140	13	BM550365
8	217.8	11.0	833	12	BF973060
9	202.8	10.2	806	10	BE277142
10	175	8.8	981	9	AL552592
11	173.2	8.7	1081	13	BM549212
12	164.6	8.3	1108	12	BE744777
13	155.8	7.8	467	9	AI820754
14	154.6	7.8	788	12	BG114850
15	146.8	7.4	741	12	BG761088
16	144.8	7.3	570	12	BG085859
17	141.4	7.1	919	12	BG104273
18	139.6	7.0	570	10	BE389884
19	136	6.9	618	10	BE407321
20	135.6	6.8	937	14	BQ222929
c	129.6	6.5	637	17	AZ939737
22	128.6	6.5	1036	12	BG476740
23	113.8	5.7	935	13	BM424081
24	109	5.5	735	10	BB650258
25	108.4	5.5	1101	13	BM464123
26	107.2	5.4	676	10	BB624152
27	104	5.2	499	10	BE385328
28	104	5.2	957	14	BQ653378
29	103.2	5.2	711	10	BB631979
30	102.6	5.2	771	12	BG397084
31	96	4.8	441	10	BE629359
c	94.8	4.8	1000	13	BM476173
33	91	4.6	661	13	BM083450
c	85	4.3	352	12	BF416476
35	81	4.1	296	14	R72114
36	80.6	4.1	703	12	BF983238
c	77	3.9	989	17	CNS02UQU
38	76	3.8	952	12	BG437263
c	74.4	3.7	890	17	AZ530768
40	74.2	3.7	1025	14	BM911907
41	73.6	3.7	905	17	AZ550256
42	73.2	3.7	843	17	AZ551618
c	73.2	3.7	931	17	BH160272
44	73	3.7	662	13	BJ495713
c	73	3.7	795	17	AZ528485

## ALIGNMENTS

RESULT 1	CNS02HJ0/c	CNS02HJ0	877 bp	DNA	linear	GSS 13-MAY-2000
LOCUS	Tetraodon nigroviridis genome survey sequence T7 end of clone					
DEFINITION	139P03 of library G from Tetraodon nigroviridis, genomic survey sequence.					
ACCESSION	AL197685					
VERSION	AL197685.1	GI:7835835				
KEYWORDS	GSS; genome survey sequence.					
SOURCE	Tetraodon nigroviridis.					
ORGANISM	Tetraodon nigroviridis					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.					
REFERENCE	1 (bases 1 to 877)					
AUTHORS	Roest-Crollius H., Jaillon O., Dasilva C., Bouneau L., Fisher C., Bernot A., Fizames C., Wincker P., Brottier P., Quetier F., Saurin W. and Weissenbach J.					
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 877)					
AUTHORS	Roest-Crollius H., Jaillon O., Dasilva C., Fizames C., Fisher C., Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and Weissenbach J.					
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis					
JOURNAL	Unpublished					









Db 315 TGGCGCAGGATGAACCAACCCATCACCATGGAATGCATATCTCTCCACTTCTGGAAC 374  
Qy 498 CGCAGCACCTACGACAGCAGCGCAACGCCACTCAGTCCCTTGGCAAGGCTACCCCGAC 557  
Db 375 CGCAGCACCTACGACAGCAGCGCAACGCCACTCAGTCCCTTGGCAAGGCTACCTGAA 434  
Qy 558 GGGGAGTCTACGACAGCAACTCTTGGTCTCCCGGAGGTGTTCTGACTCTGGGGTGCATA 617  
Db 435 GGAGGATGCTACGAGCAACTTTTGTCTCTCTCTGAGGTGTTGTGACTCTGGGTGCATA 494  
Qy 618 AGCTTGTGAGAGCAATCTGGTGAT 643  
Db 495 AGCCTGTTGGAGAACTTCTGGTGAT 520

RESULT 6  
BI830442/c  
LOCUS 603073302f1 NIH\_MGC\_119 Homo sapiens cdna clone IMAGE:5165137 5',  
DEFINITION mRNA sequence.  
ACCESSION BI830442  
VERSION BI830442.1 GI:15941992  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1017)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1410 row: d column: 02  
High quality sequence stop: 794.

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/clone\_lib="NIH\_MGC\_119"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dr primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."  
BASE COUNT 278 a 224 c 297 g 218 t  
ORIGIN

Query Match 11.88; Score 234; DB 13; Length 1017;  
Best Local Similarity 61.2%; Pred. No. 2.3e-30;  
Matches 459; Conservative 0; Mismatches 265; Indels 26; Gaps 4;

Qy 646 TGGCAATAGCAAGCAAGAACTCTG-CACTCACCCTGACT-TTTCATCTCTAGCCT 703  
Db 729 TGCTGTGTTCAAGAAATAGTACTGCCAGGCCCATGACTTTTTTCATCTGATCT 670  
Qy 704 GGCTGTGGCCGATATGCTGGTGGGTTCACAGCGGTTCACAGACCATCGTCAACCCCT 763  
Db 669 GGCCATATCTGATGATGCTGGGCGACCTATATAGATCTTGGAAATATCTTGATCATATT 610

Qy 764 GTTGAACAGTACGATACGGACGCGCAG---AGTTTCACGGTGAATATTTGATATGTCAT 820  
Db 609 GAGAAACATAGGGCTATCTCAAGCCACGCTGGCAGTTTTTGAACACACAGCCGATGACATCAT 550  
Qy 821 TGAATCGGTGATCTGTAGCTCCTTGGCTCGCTCGATTTTGCAGCCCTGCTCTCAATTTGCAGT 880  
Db 549 CGACTCCCTGTTTGTCTCTCCCTGCTGGCTCCATCTTTCAGCCCTGCTGTGATTTGCTGC 490  
Qy 881 GGACAGGTACTTACTATATCTTTTATGCCCTCCAGTACCATACATCATCATGAGGTCAGCGG 940  
Db 489 GGACCGCTACATCACCATCTTCCACGCACTCGGTTACCAACAGCATCGTGACCATCGCGCG 430  
Qy 941 GGTGGGATCATCATCATCATCTGCGGCGCTTGCACGGTGTGCAGCGTCTTCTTCTTCTTCT 1000  
Db 429 CACTGTGGTGTGCTTACGGTCACTTGCACGGGACTTGCATCACCACCATCATGGT 370  
Qy 1001 CATTACTCGGACAGTACTGCTGTATCATCTGCTCATCATCACCATGTTCTTTCACCATGCT 1060  
Db 369 GATCTTCTCCCATCATGTGCCACAGTACACCTTTCACCTCGCTGTTTCCCGCTCATGCT 310  
Qy 1061 GGCCCTCATGGCTTCTCTCTACGTCCACATGTTCTCATGTCGCGACACTGCACATCAAGAG 1120  
Db 309 GGTCTTATCTGCTGCTCTATGTGCACATGTTCTGCTGCTCGATCCACACACAGGAA 250  
Qy 1121 AATCGCGTCTCTCCGGCACCGGCACCATCGCCAAAGGGGCCAACATGAAGGTCGCCAT 1180  
Db 249 GATCTCCACCTCTCCCGA-----GCCAACATGAAGGGGCCAT 211  
Qy 1181 TACCTTGACCATACTCATTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240  
Db 210 CACTGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 151  
Qy 1241 GATATCTTACATCTTCTTGTCCCGAATCCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1300  
Db 150 CCTCTGATGACATTTCTGCCCAAGTAACCCCTACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 91  
Qy 1301 CTTGTACTCTTCTGATCATGCTGTAATCTCATCATGACCTCTCATTTATGCACTCGG 1360  
Db 90 GGTGAAGGCGCATGTTGATCATGCAATCCCGTATGACCCCTTACATATATGCTGCTGCTGCT 31  
Qy 1361 GAGCAAGAGCTGAGGAAACCTTCAAGA 1390  
Db 30 GAGCCAGAGCTCAGGACGCAATTCAAAA 1

RESULT 7  
BM550365  
LOCUS 1140 bp mRNA linear EST 20-FEB-2002  
DEFINITION AGENCOURT\_6542025 NIH\_MGC\_72 Homo sapiens cdna clone IMAGE:5549166  
5', mRNA sequence.  
ACCESSION BM550365  
VERSION BM550365.1 GI:18786509  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1140)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC/BDTD/DTP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12259 row: e column: 07  
High quality sequence stop: 622.

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/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/Note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
BASE COUNT 210 a 395 c 290 g 244 t 1 others
ORIGIN
Query Match 11.2%; Score 222.6; DB 13; Length 1140;
Best Local Similarity 59.3%; Pred. No. 1.9e-28;
Matches 397; Conservative 0; Mismatches 269; Indels 3; Gaps 1;
QY 746 GACCATCGTCATCACCCCTGTGTAACAGTAGCGGATACGGACGCGCAGAGTTTACAGGTGAA 805
Db 22 GGCGGTATCTCTCTGTGAGCGCGGTGCACGTGTGGCCGGCTGCGGTGCTGCAGCA 81
QY 806 TATTGATAATGTCATTGACTCGGTGATCTGTAGCTCTTGTCTCGCTCGATTTGCAGCCT 865
Db 82 GCTGGACAATGTCATTGACGTGATCACCTGCAGCTCCATGCTGTCAGGCTCTGTCTCT 141
QY 866 GCTCTCAATGTCAGTCGACAGGTACTTACTATCTTTTATGCTCCCTCCAGTACCATAACAT 925
Db 142 GGGCGCCATCGCGGTGACCGGTACATCTCCATCTTCTAGGCACTCGGTACCACAGCAT 201
QY 926 CATGACGGTGAGCGGGTGGGATCATATCATATGTCATCTCGGGGGCTTGCACGGGTGTC 985
Db 202 CGTGACCTTGCAGCGCGCGCGGAGCCGTGTGGCGCATCTGGGTGCGAGTGTCTCTT 261
QY 986 AGGCATCTTGTTCATCATATTTACTCGACAGTAGTCTGCTGTCATCATCTGCTCATCAAT 1045
Db 262 CAGCAGCTTCTCATCGCTACTACGACACAGTGGCGGCTTCTGCTGCTGCTGCTGCTT 321
QY 1046 GTTCTTCCACATGCTGGCCCTCATGGCTTCTCTACGTCCACATGTTCTCTCATGGCCAG 1105
Db 322 CTTCTGGCTATGCTGTGCTCATGCGCGTGTGTAGTCCACATGCTGCGCGGCGCTG 381
QY 1106 ACTGCACATCAAGAGATGCGC---GTCTCCGGGACGCGGACCATCGCCAGAGGGC 1162
Db 382 CCAGCAGCGCCAGGCGATCGCGGCTCCACAGAGCAGCGCGCGGTCCACAGGGCTT 441
QY 1163 CAACATGAAGGTGCCATTACTTGACCATCTCATTTGGGTCCTGCTGCTGCTGGGC 1222
Db 442 TGGCCTTAAGGCGTGTACCCCTACCAATCTGTGGCANTTTCTTCTCTGCTGGGG 501
QY 1223 TCCATTTCTTCCATTTGATATTTACATCTCTTTGCCAGAAATCCATCTGTGTGTG 1282
Db 502 CCCCCTTCTTCTGTCATCTCACACTCATCTGCTCTGCGCCGAGACCCACACGTGGGCTG 561
QY 1283 CTTATGTCCTCACTTTAAGTGTGATCTGATCTGATGTCATGTCATCTGATCTGATCTGAT 1342
Db 562 CATCTTCAAGAACTTCAACCTTTCTGCGCCCTCATCATCTGCAATGTCATCTGACGCC 621
QY 1343 TCTCATTTATGACATCCGAGCCAGAGCTGAGGAAACCTTCAAGAGATCATCTGTTG 1402
Db 622 CTTATCTACGCTTCCACAGCAGGAGCTCCGAGGAGCTCAAGGAGGTGCTGACATG 681
QY 1403 CTATCCTCT 1411
Db 682 CTCCTCTGCT 690
RESULT 8
BF973060
LOCUS
DEFINITION BF973060 833 bp mRNA linear EST 22-JAN-2001
602241386F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4330124 5',
mRNA sequence.
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ACCESSION BF973060.1 GI:12340275
VERSION BF973060.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 833)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1192 row: k column: 21
High quality sequence stop: 780.
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/Note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 117 a 295 c 230 g 191 t
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Query Match 11.0%; Score 217.8; DB 12; Length 833;
Best Local Similarity 60.4%; Pred. No. 1.4e-27;
Matches 449; Conservative 0; Mismatches 282; Indels 12; Gaps 5;
QY 577 TCTTGCTCTCCCGGAGGTGTTCGTGACTCTGGGGTCTATAAGCTTGTGTGAGAACATTC 636
Db 5 TGTCCATCTCTACGGGCTCTTCTCAGCCTGGGCTGTGTGAGAGACGCC 64
QY 637 TGGTGATCGTGAATAGCCAAAGAAATCTGCACCTACCCATGTACTTTTTCATCT 696
Db 65 TGGTGTGGCCACCATCGCAAGACCGGAACCTGCACCTACCCATGTACTGCTTCATCT 124
QY 697 GTAGCCTGTGTCGCGGATATGCTGGTGAGCGTTTCCAAACGGGTTCAGACCATCGTCA 756
Db 125 GCTGCTGCGCCTGTGCGGACCTGCTGCTGAGCGGAGCAACGCTGTGGAGAGCGCGTCA 184
QY 757 TCACCCCTGTGAA---CAGTACGGATACGAGCGCCAGAGTTTCACGGTGAATATTGATA 813
Db 185 TCCTCTGCTGGAGCGCGGTGCACGTGGGCGCGGCTGCGGTGTCGACAGCTGGGACA 244
QY 814 ATGTCAATGACTCGGTGATCTGTAGCTCTTCTGCTCGCTTCGATTTTGCACCTCTCTCAA 873
Db 245 ATGTCAATGACTCGGTGATCTGTAGCTCTTCTGCTCGCTTCGATTTTGCACCTCTCTCAA 304
QY 874 TTGCAGTGCAGAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATAACATCATGACGG 933
Db 305 TCGCGGTGAGCGCTTACATCTCCATCTTCTAGCAGCTGCGCTTACCACAGCATCGTGACCC 364
QY 934 TGAGCGGCTTGGGATCATCATCTGTCATCTGCGCGGCTTGCACAGGTGTCAGGCACTCT 993
Db 365 TCCCGCGGCGCGGCGGCGGCTTGGGCGCATCTGGGTGGCCAGTGTGCTCTTTCAGACGCC 424
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Matches	364;	Conservative	0;	Mismatches	227;	Indels	5;	Gaps	2;
QY	546	GGCTACCCCGAGGGGATGCTACGAGCAACTCTTCGTCTCCCCGAGGTTGTCGTGACT	605						
Db	157	GCACAACGACAGAGGAGCCGGTGCCTGGAGGTGTCCATCTCTGACGGGCTCTTTCCTCAGC	216						
QY	606	CTGGGGGTCTAATAGCTTGTGGAGAACATCTCTGGTGATCTGTGGCAATAGCCAAAGACAAG	665						
Db	217	CTGGGGCTGTGAGCTTGTGGAGAACGGGCTGTGGTGTGGCCACCACTCGCCAAAGAACCGG	276						
QY	666	AATCTCACTCAACCCATGACTTTTTCATCTGCTGAGCTGTGCTGTGGCCGATATGCTGGTG	725						
Db	277	AAGCTGCATCAACCCATGACTGCTTCATCTGCTGTGGCTGTGGACCTGCTGGTG	336						
QY	726	AGCGTTTCCAAAGGGTCAGAGACCACTGCTCATCACCTCTTTGAA---CAGTACGGATACG	782						
Db	337	AGCGGAGCAACGCTGTGGAGAGCGGCTCATCTCTCTGTGGAGCCGGTGCACCTGGTG	396						
QY	783	GAGCGCAGAGTTTACGGTGAATATTGATTAATGTCATTGACATGACATGCTGTGATGCTCTC	842						
Db	397	GCCCGGGCTGGGTGCTGCAGCAGCTGGCAATATGTCATGACGTGATCATCCTGCAGCTCC	456						
QY	843	TGCTGCGCTCGATTTGACGCTGCTCAATTTGACGTGGACAGGTAATTTACTATCTTT	902						
Db	457	ATGCTGTCCAGGCTCTGCTTCTGGGCGCATGCGCGTGGACCGCTACATCTCCATCTTC	516						
QY	903	TATGCCCTCAGTACCATAACATCATGACGGTGGAGCGGTGGATCATCATCATCTGTC	962						
Db	517	TAGGCACTGGCTACCAACAGCATCTGACCTGCCGCGGGCGGAGCGGCTGGCGGC	576						
QY	963	ATCTGGGCGGCTTGCACGCTGTGACGATCTTTGTTTCATCATTTTACCTGCGACAGTACTGT	1022						
Db	577	ATCTGGGTGGCCAGTGTGCTCTTTCAGCACGCTCTTCATCGCCTACTACGACACGCTGGC	636						
QY	1023	GTCATCATCTGCTCATCACCATGTTCTTACCATCTGCTGGCCCTCATGCTTCTCTCTAC	1082						
Db	637	GTCCTCTGCTGCTGCTGCTGCTTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC	696						
QY	1083	GTCCACATGTTCTCATGCCAGACTGACATCAAGAGAAATGCGCGTCTCTCCCGG	1138						
Db	697	GTCCACATGCTGCC---GGGCGCTGCACGACGCCAGGCGATCGCCGGTCCACAGAG	750						
RESULT	10								
LOCUS	AL552592								
DEFINITION	AL552592 LRI_NFL006_PL2 Homo sapiens CDNA clone CS0DI067YJ14 5								
ACCESSION	AL552592								
VERSION	AL552592.1								
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 (bases 1 to 981)								
AUTHORS	Li, W. B., Gruber, C., Jessee, J., and Polayes, D.								
TITLE	Full-length cDNA libraries and normalization								
JOURNAL	Unpublished (2001)								
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequenage BP 191 91006 EVRY cedex - France Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.								
FEATURES	Location/Qualifiers								
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	/organism="Homo sapiens"								
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	/clone="CS0DI067YJ14"								
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	/tissue_type="placenta"								
	/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA								
	was primed with a NotI-oligo(dT) primer. Five prime end								
	enriched, double-stranded cDNA was digested with Not I and								
BASE COUNT	121 a 270 c 248 g 167 t								
ORIGIN									
Query Match	10.2%;								
Best Local Similarity	61.1%;								
	Pred. No. 5e-25;								
	Score 202.8; DB 10; Length 806;								

cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL : <http://fulllength.invitrogen.com>

BASE COUNT	171 a	299 c	327 g	179 t	5 others
ORIGIN					

Query Match 8.8%; Score 175; DB 9; Length 981;  
Best Local Similarity 60.3%; Pred. NO. 2.6e-20;  
Matches 319; Conservative 3; Mismatches 203; Indels

[illegible]

RESULT 11	
BM549212	
LOCUS	1081 bp
DEFINITION	linear mRNA
	AGENCOURT_6558414 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548486
	5', mRNA sequence.
ACCESSION	BM549212
VERSION	BM549212.1
KEYWORDS	GI:18784430
SOURCE	EST.
	human.

ORGANISM	Human:
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 1081)
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: ATCC/DCTD/DTF CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLAM12257 row: h column: 23  
 High quality sequence stop: 707.

BASE COUNT	171 a	347 c	348 g	211 t	4 others
ORIGIN					

Query Match	8.7%	Score 173.2	DB 13	Length 1081	
Best Local Similarity	60.6%	Pred. No. 5.le-20			
Matches 335	Conservative 0	Mismatches 211	Indels 7	Gaps 3	
QY	546	GGCTACCCCGACGGGGATGCTACGAGCAACTCTTCGTCCTCCCGGAGGTGTCGTGACT	605		
DB	364	GCCAAACAGACAGAGCCGGTCTGGAGGTGTCATCTCTGACGGGCTCTTCTCTCAGC	423		
QY	606	CTGGGGCTATAAGCTTCTCGGAAACATTTCTGTGTATCTGTGGCAATAGCCAAAGAACAG	665		
DB	424	CTGGGGCTGAGGAGCTTGGTGGAGACGCGTGTGTGGCCACCATCGCCCAAGACCGG	483		
QY	666	AATCTGACATCACCCATGTACTTTTTCATCTGTATGACCTGTGTGGCGGATATGCTGTGT	725		
DB	484	AAGCTGACATCACCCATGTACTTCTTCATCTGTCTGGCCTTGTGGACCTGTGTGTGT	543		
QY	726	AGCGTTTCCAAACGGGTACAGACCATCGTTCATCACCCCTGTGAA--CAGTACGATACG	782		
DB	544	AGCGGAGCAACGTCGTGGAGCGGCCGTATCTCTCTGTGGAGCGCGGTGCACTGGTG	603		
QY	783	GACGCGCAGAGTTTTCACGGTGAATATTGATAATTCATTCGCTCGGTGATCTGTAGCTCC	842		
DB	604	GCCCGGGCTCGGTGTCGACGAGCTGGCAATGTCATTCGACGTGATCACTCGCAGCTCC	663		
QY	843	TTGCTCGCCGTCGATTTTTCGACGCTGCTCTCAATTCGACGTGGACAGGTACTTTTACATCTTT	902		
DB	664	ATGCTGTCCAGCCTCTGCTTCTTCTGGGGCCCATGCGCGTGGACCACTACATCTCCATCTTC	723		
QY	903	TATGCCCTCCAGTACCATATACATGACGCTGAGCGGGTGGGATCATCATCAGTTGC	962		
DB	724	TAGCCACTTGGCTTACCACAGCATGTCGACCCCTGCGCGGGCGCGGAGCGGCTTGGCGGCC	783		
QY	963	ATCTGGCGGCTTTGACGCTGTGAGGATCTTTGTTTCATCATTTACTCGGACAGTACTGCT	1022		
DB	784	ATCTGGGTGCCAGTGTGCTTTCAGACACGCTCTCTATCGCCTACTAGCACCGTGGCC	843		
QY	1023	GTCAATCATGTG---CTCATCACAGTTCCTTCACCAATGCTGGCCCTCATGCGGCTCT-CT	1078		
DB	844	CGTCTGNNCTGTGCCCTCGTGGTCTTCTTCTCGCTATGCTGGNGCTCATGCGCCGCT	903		
QY	1079	CTACGTCCACATG	1091		
DB	904	GTACGTCCACATG	916		
RESULT 12	BE744777	1108 bp	mRNA	linear	EST 15-SEP-2000
LOCUS	601573166F1	NIH_MGC_9	Homo sapiens	cdna clone	IMAGE:3834185 5',
DEFINITION	mRNA sequence.				
ACCESSION	BE744777				
VERSION	BE744777.1				
KEYWORDS	GI:10158756				
	EST				







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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:31 ; Search time 51 Seconds  
(without alignments)  
867.435 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGHMHTSLHFNWST.....FKREICCYPLGGCLDLSSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	100.0	332	23	Feline melanocortin
2	1685	97.5	332	23	Canine melanocortin
3	1659.5	96.0	332	18	Melanocortin-4 rec
4	1659.5	96.0	332	19	Melanocortin-4 rec
5	1659.5	96.0	332	19	Human melanocortin
6	1659.5	96.0	332	20	Human MC4 protein.
7	1659.5	96.0	332	21	A human melanocort
8	1659.5	96.0	332	21	Synthetic labeled
9	1659.5	96.0	332	22	Amino acid sequenc
10	1653.5	95.7	332	21	Human G protein co

11	1653.5	95.7	332	23	AAE15746	Human melanocortin
12	1648.5	95.4	332	21	AAE02857	Human G protein co
13	1645.5	95.2	332	21	AAE94301	Rhesus monkey mela
14	1632.5	94.5	332	21	AAE83182	Melanocortin recep
15	1617.5	93.6	332	21	AAE87415	Melanocortin-4 rec
16	1613.5	93.4	332	19	AAW37831	Human melanocortin
17	1613.5	93.4	332	20	AAW42377	Homo sapiens mutan
18	1613.5	93.4	332	20	AAW87869	Human melanocortin
19	1611.5	93.3	332	19	AAW42378	Homo sapiens mutan
20	1604.5	92.9	332	19	AAW42379	Homo sapiens mutan
21	1465	84.8	311	22	AAU08750	Human melanocortin
22	1407	81.4	293	21	AAE83184	Melanocortin recep
23	1266	73.3	248	21	AAE78931	Porcine melanocort
24	1261	73.0	248	22	AAU08751	Porcine melanocort
25	1250	72.3	248	21	AAE78932	Porcine melanocort
26	1047	60.6	325	16	AAE79501	Rat melanocortin r
27	1030	59.6	325	19	AAE37833	Mouse melanocortin
28	1030	59.6	325	20	AAW87870	Mouse melanocortin
29	1027	59.4	325	18	AAW19705	Melanocortin-5 rec
30	1027	59.4	325	19	AAE79688	Melanocortin-5 rec
31	1027	59.4	325	19	AAW41067	Mouse melanocortin
32	1027	59.4	325	19	AAE33725	Mouse melanocortin
33	1027	59.4	325	20	AAE92443	Mouse MC5 protein.
34	1027	59.4	325	21	AAE18770	A human melanocort
35	1024.5	59.3	325	21	AAE94266	Rhesus monkey mela
36	1023.5	59.2	325	16	AAE79502	Human melanocortin
37	1000.5	57.9	323	21	AAE94427	Rhesus monkey mela
38	1000.5	57.9	323	22	AAE60968	Murine melanocorti
39	1000.5	57.9	323	23	AAE20595	Mus musculus melan
40	997.5	57.7	325	15	AAE49726	Sequence of a poly
41	988.5	57.2	360	23	AAU95520	Human olfactory an
42	987.5	57.1	360	18	AAW19703	Melanocortin-3 rec
43	987.5	57.1	360	19	AAE79686	Melanocortin-3 rec
44	987.5	57.1	360	19	AAE33723	Human melanocortin
45	987.5	57.1	360	20	AAE92441	Human MC3 protein.

ALIGNMENTS

RESULT 1

AAU76427

ID AAU76427 standard; Protein; 332 AA.

XX AC AAU76427;

XX DT 08-MAY-2002 (first entry)

XX DE Feline melanocortin 4 receptor (MC4R).

XX KW Melanocortin 4 receptor; MC4R; G-protein coupled; receptor; cat;

XX KW appetite; metabolic disorder; cachexia; anorexia;

XX KW weaning-induced inappetence; growth; diabetes; cancer; renal failure;

XX KW cardiac disease; endotoxaemia; fever; hepatic lipidosis; infection;

XX KW inflammation; post partum sow; dairy cow; livestock; poultry;

XX KW shipping stress; crowding stress; obesity; vaccine.

XX OS Felidae.

XX PN EP1167386-A1.

XX PD 02-JAN-2002.

XX PF 26-JUN-2001; 2001EP-0305509.

XX PR 26-JUN-2000; 2000US-213909P.

XX PA (PFIZ ) PFIZER PROD INC.

XX PI Hickman MA, Houseknecht KL, Robertson AS;

XX DR WPI; 2002-156598/21.

XX DR N-PSDB; ABK15577.

XX Novel canine or feline melanocortin 4 receptor polypeptide for  
PT screening modulator compounds useful for treating cachexia, anorexia,  
PT diabetes and cancer  
XX  
XX  
PS Claim 3; Fig 3; 73pp; English.  
XX  
XX The invention describes a substantially pure canine or feline  
CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be  
CC used in the treatment of appetite-related or metabolic disorders  
CC including cachexia, anorexia or weaning-induced inappetence and growth  
CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,  
CC fever, hepatic lipidosis, infection or inflammation, in a post partum  
CC sow, dairy cow, companion animal, livestock animal, poultry animal,  
CC animal suffering from shipping or crowding stress, lactating animal,  
CC obese animal or a gravid animal. (I) is useful in the generation of  
CC antibodies, as reagents in diagnostic assays, identification of other  
CC cellular gene products involved in the regulation of appetite in animals,  
CC as reagents in assays for screening for compounds that can be used in the  
CC treatment of appetite disorders in animals. A ligand of MC4R is useful  
CC for elaborating the biological function of MC4R gene product and for  
CC ameliorating appetite disorders and metabolic disorders, in animals. This  
CC is the amino acid sequence of the feline melanocortin 4 receptor (MC4R),  
CC a G-protein coupled receptor described in the method of the invention.  
XX  
XX Sequence 332 AA;  
Query Match 100.0%; Score 1728; DB 23; Length 332;  
Best Local Similarity 100.0%; Pred. No. 9.3e-182;  
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSTHHGMHTSLHFWNRSTYGPNSASESLGKGYSDGCVQQLFVSPVFTLGVISLL 60  
DB 1 MNSTHHGMHTSLHFWNRSTYGPNSASESLGKGYSDGCVQQLFVSPVFTLGVISLL 60  
QY 61 ENILVIVAIAKNKLNHSPWFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFVN 120  
DB 61 ENILVIVAIAKNKLNHSPWFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFVN 120  
QY 121 IDNVDSVICSLLASICSLLSIADRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180  
DB 121 IDNVDSVICSLLASICSLLSIADRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180  
QY 181 GVLFTIYSDSSAVIICLTMTFFMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
DB 181 GVLFTIYSDSSAVIICLTMTFFMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
QY 241 MKGATLTILIGVFCVWVWAPFLHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
DB 241 MKGATLTILIGVFCVWVWAPFLHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
QY 301 IYALRSQELRKTFRKEIICCYPLGGCLDLSRY 332  
DB 301 IYALRSQELRKTFRKEIICCYPLGGCLDLSRY 332  
RESULT 2  
AAU76428  
ID AAU76428 standard; Protein; 332 AA.  
XX  
XX AAU76428;  
AC  
XX  
XX  
DT 08-MAY-2002 (first entry)  
XX  
XX Canine melanocortin 4 receptor (MC4R).  
XX  
XX Melanocortin 4 receptor; MC4R; G-protein coupled receptor; dog;  
KW appetite; metabolic disorder; cachexia; anorexia;  
KW weaning-induced inappetence; growth; diabetes; cancer; renal failure;  
KW cardiac disease; endotoxaemia; fever; hepatic lipidosis; infection;  
KW inflammation; post partum sow; dairy cow; livestock; poultry;  
KW shipping stress; crowding stress; obesity; vaccine.

OS Canidae.  
XX  
PN EPI167386-A1.  
XX  
PD 02-JAN-2002.  
XX  
XX 26-JUN-2001; 2001EP-0305509.  
PF  
XX 26-JUN-2000; 2000US-213909P.  
PR  
XX (PFIZ ) PFIZER PROD INC.  
PA  
XX Hickman MA, Houseknecht KL, Robertson AS;  
PI WPI; 2002-156598/21.  
XX N-PSDB; ABK15578.  
DR  
XX Novel canine or feline melanocortin 4 receptor polypeptide for  
PT screening modulator compounds useful for treating cachexia, anorexia,  
PT diabetes and cancer  
XX  
XX Claim 22; Fig 4; 73pp; English.  
XX  
XX The invention describes a substantially pure canine or feline  
CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be  
CC used in the treatment of appetite-related or metabolic disorders  
CC including cachexia, anorexia or weaning-induced inappetence and growth  
CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,  
CC fever, hepatic lipidosis, infection or inflammation, in a post partum  
CC sow, dairy cow, companion animal, livestock animal, poultry animal,  
CC animal suffering from shipping or crowding stress, lactating animal,  
CC obese animal or a gravid animal. (I) is useful in the generation of  
CC antibodies, as reagents in diagnostic assays, identification of other  
CC cellular gene products involved in the regulation of appetite in animals,  
CC as reagents in assays for screening for compounds that can be used in the  
CC treatment of appetite disorders in animals. A ligand of MC4R is useful  
CC for elaborating the biological function of MC4R gene product and for  
CC ameliorating appetite disorders and metabolic disorders, in animals. This  
CC is the amino acid sequence of the canine melanocortin 4 receptor (MC4R),  
CC a G-protein coupled receptor described in the method of the invention.  
XX  
XX Sequence 332 AA;  
Query Match 97.5%; Score 1685; DB 23; Length 332;  
Best Local Similarity 97.6%; Pred. No. 5.1e-177;  
Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MNSTHHGMHTSLHFWNRSTYGPNSASESLGKGYSDGCVQQLFVSPVFTLGVISLL 60  
DB 1 MNSTHHGMHTSLHFWNRSTYGPNSASESLGKGYSDGCVQQLFVSPVFTLGVISLL 60  
QY 61 ENILVIVAIAKNKLNHSPWFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFVN 120  
DB 61 ENILVIVAIAKNKLNHSPWFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFVN 120  
QY 121 IDNVDSVICSLLASICSLLSIADRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180  
DB 121 IDNVDSVICSLLASICSLLSIADRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180  
QY 181 GVLFTIYSDSSAVIICLTMTFFMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
DB 181 GVLFTIYSDSSAVIICLTMTFFMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
QY 241 MKGATLTILIGVFCVWVWAPFLHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
DB 241 MKGATLTILIGVFCVWVWAPFLHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
QY 301 IYALRSQELRKTFRKEIICCYPLGGCLDLSRY 332  
DB 301 IYALRSQELRKTFRKEIICCYPLGGCLDLSRY 332  
RESULT 3

```

AAW19704
ID AAW19704 standard; Protein; 332 AA.
XX
AC AAW19704;
XX
DT 19-AUG-1997 (first entry)
XX
DE Melanocortin-4 receptor.
XX
KW Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;
KW pro-opiomelanocortin; adrenal cortical function; behaviour; learning;
KW memory; cardiovascular system; analgesia; thermoregulation; prolactin;
KW neurohumoral agent; biogenic amine.
XX
OS Homo sapiens.
XX
XX US5622860-A.
XX
PD 22-APR-1997.
XX
XX 17-FEB-1994; 94US-0200711.
XX
PR 17-FEB-1994; 94US-0200711.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Gantz I, Yamada T;
XX
DR WPI; 1997-244394/22.
DR N-PSDB; AAT68790.
XX
XX Nucleic acid molecules encoding melanocortin receptors - useful to
PT transfect mammalian cells lacking endogenous receptors to induce
PT their expression
XX
PS Claim 4; Column 43-46; 58pp; English.
XX
AAW19703-W19707 represent the human and mouse melanocortin (MC)
CC receptors. This sequence represents the MC4R, expressed primarily in
CC brain, but absent in the adrenal cortex, melanocytes and placenta. The
CC gene encoding this sequence is located at chromosome locus 18q21.3. MCs
CC are products of pro-opiomelanocortin post-translational processing, and
CC are known to have a broad array of physiological actions. MCs are known
CC to have effects on adrenal cortical functions and on melanocytes, as well
CC as affecting behaviour, learning, memory, control of the cardiovascular
CC system, analgesia, thermoregulation and the release of other neurohumoral
CC agents (such as prolactin and biogenic amines). The nucleic acids can be
CC used to transfect mammalian cells lacking endogenous MC receptors to
CC induce their expression. These sequences can also be used to screen and
CC identify drugs which specifically react with MCRs on the surface of a
CC cell. The drugs can then be used for treating diseases which have MCRs
CC implicated as one of their causes. Vectors containing these sequences can
CC also be used to treat the diseases.
XX
SQ Sequence 332 AA;
Query Match 96.0%; Score 1659.5; DB 18; Length 332;
Best Local Similarity 96.7%; Pred. No. 3.3e-174;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 1 MNSTHHGHTSLHFNWRSYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
DB 2 VNST-HRGMHTSLHLNWRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
QY 61 ENILVIVAIKNNLHSPMTFFTCSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
DB 61 ENILVIVAIKNNLHSPMTFFTCSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASCSLLSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
DB 121 IDNVDSVICSSLLASCSLLSTAVDRYFTIFALQYHNMTVRRVGIISCIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLTMTFFTMALMASLYVHMFMLARLHKRIAVLPGTGAIROGAN 240

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181 GILFIYSDSSAVIICLTMTFFTMALMASLYVHMFMLARLHKRIAVLPGTGAIROGAN 240
QY 241 MKGAITLTILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
DB 241 MKGAITLTILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
QY 301 IYALRSOELRKRTFKEIICCYPLGGICDLSSRY 332
DB 301 IYALRSOELRKRTFKEIICCYPLGGICDLSSRY 332
RESULT 4
AAW79687
ID AAW79687 standard; Protein; 332 AA.
XX
XX AAW79687;
XX
DT 17-DEC-1998 (first entry)
XX
DE Melanocortin-4 receptor.
XX
KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain;
KW adrenal cortex; melanocyte; placenta.
XX
OS Homo sapiens.
XX
PN US5817787-A.
XX
PD 06-OCT-1998.
XX
XX 23-APR-1997; 97US-0842045.
XX
PR 17-FEB-1994; 94US-0200711.
PR 27-JUN-1996; 96US-0672109.
PR 23-APR-1997; 97US-0842045.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
PI Gantz I, Yamada T;
XX
DR WPI; 1998-556471/47.
DR N-PSDB; AAV62352.
XX
XX DNA encoding melanocortin-5 receptor - useful in hybridisation
PT assays for melanocortin-5 receptor nucleic acids
XX
XX Disclosure; Column 43-46; 58pp; English.
XX
XX The present sequence represents the human melanocortin-4 (MC4) receptor,
XX the gene of which has been localised to chromosome 18q21.3. This
XX receptor is activated by both the amino and carboxyl terminal end amino
XX acids of melanocortins and has been found to be expressed primarily in
XX the brain and is absent from the adrenal cortex, melanocytes and
XX placenta. The DNA sequence that produces this polypeptide was identified
XX by using oligonucleotides constructed from previously identified
XX receptors MC1 and MC3, this was performed by using these oligonucleotides
XX to search genomic DNA for other members of the receptor family. These
XX genes and their products may be used to provide therapeutic vehicles for
XX the treatment of processes involving the function of melanocortin
XX receptors.
XX
SQ Sequence 332 AA;
Query Match 96.0%; Score 1659.5; DB 19; Length 332;
Best Local Similarity 96.7%; Pred. No. 3.3e-174;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 1 MNSTHHGHTSLHFNWRSYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
DB 2 VNST-HRGMHTSLHLNWRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
QY 61 ENILVIVAIKNNLHSPMTFFTCSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

```





PS Example 11; Page 71; 120pp; English.

CC New methods are described by which membrane polypeptides can be  
CC labelled. The method comprises chemoselective chemical ligation of  
CC the membrane polypeptide which is incorporated in a lipid matrix,  
CC and a ligation label. Both contain an amino acid having an  
CC unprotected reactive group that together undergo chemoselective  
CC ligation to form a covalent bond. The method can be used to label  
CC folded polypeptides embedded in a lipid membrane, by treating the  
CC polypeptide with a reagent that cleaves specifically adjacent to an  
CC amino acid with an unprotected reactive group and then ligating the  
CC cleaved polypeptide with the ligation label. The ligation label can  
CC be a chromophore, thus ligand binding to membrane bound polypeptides  
CC can be detected by contacting a membrane bound polypeptide comprising  
CC a chromophore, with the ligand under investigation and screening for  
CC binding in an assay characterized by detecting fluorescence resonance  
CC energy transfer (FRET) between the chromophore and a second  
CC chromophore, the chromophores comprising a donor and acceptor pair of  
CC a resonance energy transfer system. The methods are used for lipid  
CC matrix-assisted chemical ligation and synthesis of membrane  
CC polypeptides. Labeled membrane polypeptides are used to detect ligand  
CC binding and the identification of receptor domains, e.g. for  
CC structure/activity studies. They can also be used in drug screening,  
CC used for fluorescent resonance energy transfer (FRET) analysis of  
CC previously inaccessible membrane polypeptides. The method allows  
CC site-specific incorporation of labels during polypeptide synthesis  
CC and analysis of previously inaccessible membrane proteins. A  
CC Melanocortin receptor MC4 which also comprises a Factor Xa cleavage  
CC site (AAV83182) can be cleaved with Factor Xa to give a  
CC C-terminal alpha-thioester modified MC4 receptor ligation label  
CC (AAV83183) and an MC4 receptor membrane polypeptide cleavage product  
CC (AAV83184). Chemical ligation of cleaved MC4 in alternative  
CC membrane patches or micelles to an MC4 ligation label produces this  
CC synthetic labeled MC4 product (AAV83185).

XX Sequence 332 AA;

Query Match 96.0%; Score 1659.5; DB 21; Length 332;  
Best Local Similarity 96.7%; Pred. No. 3.3e-174;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGHMTSLHFWNRSTYCPHNSASESLGKGYSDGCGYQQLFVSPFVTLGVISLL 60  
DB 2 VNST-HRGMHTSLHLWNRSYRLHNSASESLGKGYSDGCGYQQLFVSPFVTLGVISLL 60  
QY 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120  
DB 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
DB 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
QY 181 GVLFTIYDSSAVIICLTIMFTMLMALMASLVHFMFLMARLHKRIAVLPGGTGTROGAN 240  
DB 181 GVLFTIYDSSAVIICLTIMFTMLMALMASLVHFMFLMARLHKRIAVLPGGTGTROGAN 240  
QY 241 MKGAILTLILIGVFFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
DB 241 MKGAILTLILIGVFFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
QY 301 IYALRSQELRKTFKEIICYPGLGLCDLSSRY 332  
DB 301 IYALRSQELRKTFKEIICYPGLGLCDLSSRY 332

RESULT 9

AAB68490

ID AAB68490 standard; Protein; 332 AA.

XX AC AAB68490;

XX

DT 23-JUL-2001 (first entry)

XX Amino acid sequence of a human melanocortin-4 receptor (MC-R4).

XX Human: melanocortin-4 receptor; MC-R4; transgenic animal; body weight;  
XX food intake; obesity; diabetes; anorexia; cachexia; cancer;  
XX sexual dysfunction; pain; impaired memory; neuronal regeneration;  
XX neuropathy; growth disorder; growth hormone;  
XX insulin-like growth factor-1.

OS Homo sapiens.

XX WO200133956-A1.

XX 17-MAY-2001.

XX 13-NOV-2000; 2000WO-US31061.

XX 12-NOV-1999; 99US-0165074.

XX (MERI ) MERCK & CO INC.

XX Van Der Ploeg LHT, Chen AS, Chen HY, Forrest MJ, MacIntyre DE;  
XX Metzger JM, Palya OC, Feighner SD, Hreniuk D;  
XX N-PSDB; AAF85465.

XX WPI; 2001-343541/36.

XX New transgenic animal with non-functional gene for melanocortin-4  
XX receptor, useful for identifying specific modulators, potentially used  
XX for treating obesity or diabetes -  
XX Disclosure; Fig 2; 58pp; English.

XX The present sequence represents a human melanocortin-4 receptor (MC-R4).  
XX The specification describes transgenic non-human animals whose somatic  
XX and germ cells contain at least one non-functional gene for MC-4R  
XX protein. The transgenic animals, or cells derived from them, are used  
XX to screen for compounds that modulate MC-4R. These modulators are  
XX potentially useful for regulating body weight and food intake and  
XX treatment of associated diseases, obesity; diabetes; anorexia; cachexia;  
XX cancer; sexual dysfunction; pain; impaired memory or neuronal  
XX regeneration; neuropathy; growth disorders linked to growth hormone  
XX and insulin-like growth factor-1. They can also be used to study MC-4R  
XX expression and activity.

XX Sequence 332 AA;

Query Match 96.0%; Score 1659.5; DB 22; Length 332;  
Best Local Similarity 96.7%; Pred. No. 3.3e-174;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGHMTSLHFWNRSTYCPHNSASESLGKGYSDGCGYQQLFVSPFVTLGVISLL 60  
DB 2 VNST-HRGMHTSLHLWNRSYRLHNSASESLGKGYSDGCGYQQLFVSPFVTLGVISLL 60  
QY 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120  
DB 61 ENILVIVATAKNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
DB 121 IDNVDSVTCSSLLASICSLLSIADVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
QY 181 GVLFTIYDSSAVIICLTIMFTMLMALMASLVHFMFLMARLHKRIAVLPGGTGTROGAN 240  
DB 181 GVLFTIYDSSAVIICLTIMFTMLMALMASLVHFMFLMARLHKRIAVLPGGTGTROGAN 240  
QY 241 MKGAILTLILIGVFFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
DB 241 MKGAILTLILIGVFFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
QY 301 IYALRSQELRKTFKEIICYPGLGLCDLSSRY 332







Db 121 IDNVDSVICSLLASCSLLSIADVRYTFIFYALQYHNIMTVKRVGISISCIWAACVTS 180  
 Qy 181 GVLFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGIRQGAN 240  
 Db 181 GILFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGIRQGAN 240  
 Qy 241 MKGAIITLILIGVFWVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 Db 241 MKGKITLILIGVFWVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 Qy 301 IYALRSQELKRTFKEIICCPYPLGGLDLSRY 332  
 Db 301 IYALRSQELKRTFKEIICCPYPLGGLDLSRY 332

RESULT 13  
 AAY94301  
 ID AAY94301 standard; Protein; 332 AA.  
 AC AAY94301;  
 XX  
 XX 04-AUG-2000 (first entry)  
 DT  
 DE Rhesus monkey melanocortin-4 receptor protein.  
 XX  
 XX Rhesus monkey; rhodopsin; G-protein coupled receptor; anorectic;  
 KW melanocyte stimulating hormone; melanocortin receptor; obesity.  
 KW  
 XX Macaca mulatta.  
 OS  
 XX WO200027863-A1.  
 PN  
 XX 18-MAY-2000.  
 PD  
 XX  
 XX 05-NOV-1999; 99WO-US25767.  
 PF  
 XX  
 XX 09-NOV-1998; 98US-0107721.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX MacNeil DJ, Weinberg DH, Van Der Ploeg LHT;  
 PI WPI; 2000-376480/32.  
 XX N-PSDB; AAA26972.  
 DR  
 XX Novel DNA encoding rhesus monkey melanocortin 4 receptor protein,  
 PT recombinant vectors and host cells, useful in methods for identifying  
 PT selective agonists and antagonists -  
 XX  
 XX Claim 27; Page 35; 53pp; English.

The present sequence is the rhesus monkey melanocortin-4 receptor protein (MC-4R). Melanocortin receptors belong to the rhodopsin sub-family of G-protein coupled receptors. They bind and are activated by peptides such as alpha-, beta-, or gamma-melanocyte stimulating hormones derived from the pro-opiomelanocortin gene and they are believed to mediate a wide range of physiological functions. The rhesus MC-4R gene was isolated by PCR using a series of four oligonucleotides (AAA26973-A26976) based on the human MC-4R gene sequence and designed to incorporate a restriction enzyme site for cloning into the expression vector pCI-neo. The recombinant vector was transformed into DH5a cells in preparation for DNA sequencing. The MC-4R gene expression vector for expression in host cells. The subcellular membrane fractions will comprise either wild-type or mutant forms of rhesus MC-4R at enhanced levels and can be used in assays to identify ligand binding, activators and modulators, agonists and antagonists of MC-4R. This will allow for selection of compounds that are active for the rhesus receptor in vitro and will allow the selection of novel drugs to treat obesity.

Sequence 332 AA;

Query Match 95.2%; Score 1645.5; DB 21; Length 332;  
 Best Local Similarity 95.8%; Pred. No. 1.2e-172;  
 Matches 318; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MNSFHHGHTSLHFWRSTYGPHSNASESLGKGYSDGGCYEQLFVSEVFTLGVISLL 60  
 Db 2 VNST-HRGMASLHLNRRSSHLNASESLGKGYSDGGCYEQLFVSEVFTLGVISLL 60  
 Qy 61 ENILVIVAIANKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFVN 120  
 Db 61 ENILVIVAIANKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFVN 120  
 Qy 121 IDNVDSVICSLLASCSLLSIADVRYTFIFYALQYHNIMTVKRVGISISCIWAACVTS 180  
 Db 121 IDNVDSVICSLLASCSLLSIADVRYTFIFYALQYHNIMTVKRVGISISCIWAACVTS 180  
 Qy 181 GVLFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGIRQGAN 240  
 Db 181 GILFIYSDSSAVIICLTITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGIRQGAN 240  
 Qy 241 MKGAIITLILIGVFWVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 Db 241 MKGAIITLILIGVFWVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
 Qy 301 IYALRSQELKRTFKEIICCPYPLGGLDLSRY 332  
 Db 301 IYALRSQELKRTFKEIICCPYPLGGLDLSRY 332

RESULT 14  
 AAY83182  
 ID AAY83182 standard; protein; 332 AA.  
 XX  
 AC AAY83182;  
 XX  
 DT 24-JUL-2000 (first entry)  
 XX  
 DE Melanocortin receptor MC4 comprising Factor Xa cleavage site.  
 XX  
 KW Membrane polypeptide; lipid matrix; synthesis; ligation;  
 KW chemoselective ligation; fluorescence resonance energy transfer;  
 KW FRET; Chromophore; ligand; receptor domain; drug screening;  
 KW diagnosis; ion channel; melanocortin receptor; MC4.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO200012536-A2.  
 XX  
 XX 09-MAR-2000.  
 PD  
 XX 26-AUG-1999; 99WO-US19542.  
 PF  
 XX 31-AUG-1998; 98US-0144964.  
 PR 05-MAR-1999; 99US-0263971.  
 XX  
 XX (GRYP-) GRYPHON SCI.  
 XX  
 XX Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;  
 PI WPI; 2000-270792/23.  
 XX  
 XX Selectively labeled membrane peptides, useful e.g. for detecting ligand  
 PT binding to receptors and in drug screening, are prepared, in lipid  
 PT matrix, by reaction between amino acid residues  
 XX  
 XX Example 11; Page 68-69; 120pp; English.  
 XX  
 CC New methods are described by which membrane polypeptides can be  
 CC labelled. The method comprises chemoselective chemical ligation of  
 CC the membrane polypeptide which is incorporated in a lipid matrix,  
 CC and a ligation label. Both contain an amino acid having an  
 CC unprotected reactive group that together undergo chemoselective

CC ligation to form a covalent bond. The method can be used to label  
 CC folded polypeptides embedded in a lipid membrane, by treating the  
 CC polypeptide with a reagent that cleaves specifically adjacent to an  
 CC amino acid with an unprotected reactive group and then ligating the  
 CC cleaved polypeptide with the ligation label. The ligation label can  
 CC be a chromophore, thus ligand binding to membrane bound polypeptides  
 CC can be detected by contacting a membrane bound polypeptide comprising  
 CC a chromophore, with the ligand under investigation and screening for  
 CC binding in an assay characterized by detecting fluorescence resonance  
 CC energy transfer (FRET) between the chromophore and a second  
 CC chromophore, the chromophores comprising a donor and acceptor pair of  
 CC a resonance energy transfer system. The methods are used for lipid  
 CC matrix-assisted chemical ligation and synthesis of membrane  
 CC polypeptides. Labeled membrane polypeptides are used to detect ligand  
 CC binding and the identification of receptor domains, e.g. for  
 CC structure/activity studies. They can also be used in drug screening,  
 CC selection or design, and for diagnosis. The methods are particularly  
 CC used for fluorescent resonance energy transfer (FRET) analysis of  
 CC previously inaccessible membrane polypeptides. The method allows  
 CC site-specific incorporation of labels during polypeptide synthesis  
 CC and analysis of previously inaccessible membrane proteins. This  
 CC sequence is the sequence of Melanocortin receptor MC4 which also  
 CC comprises a Factor Xa cleavage site. Cleavage with Factor Xa gives  
 CC a C-terminal alpha-thioester modified MC4 receptor ligation label  
 CC (AAV83183) and an MC4 receptor membrane polypeptide cleavage product  
 CC (AAV83184). Chemical ligation of cleaved MC4 in alternative  
 CC membrane patches or micelles to an MC4 ligation label produces the  
 CC synthetic labeled MC4 product (AAV83185).  
 XX  
 SQ Sequence 332 AA;

Query Match 94.5%; Score 1632.5; DB 21; Length 332;  
 Best Local Similarity 95.5%; Pred. No. 3.1e-171;  
 Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
 Db 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPFVTLGVISLL 60  
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 2 VNST-HRGHMTSLHLNRRSSYRLHNSNASESLGKGYEGRCYEQLFVSPFVTLGVISLL 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 ENILVIVATKNNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDQSFVN 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 ENILVIVATKNNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDQSFVN 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 121 IDNVDSVCSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGGIIICWAACTVS 180  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 121 IDNVDSVCSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGGIIICWAACTVS 180  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTROGAN 240  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 181 GILFIYSDSSAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTROGAN 240  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 241 MKGATLTILIGVFVVCWAPFELHIFVYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 241 MKGATLTILIGVFVVCWAPFELHIFVYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 301 IVALRSQELRKTFFKEIICYPGLGCLDLSRY 332  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 301 IVALRSQELRKTFFKEIICYPGLGCLDLSRY 332  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15  
 AAY87415  
 ID AAY87415 standard; protein; 332 AA.  
 XX  
 AC AAY87415;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE Melanocortin-4 receptor (MC4-R).  
 XX  
 KW Melanocortin-4 receptor; MC4-R; Inhibitor; addictive behaviour;  
 KW drug addiction; cocaine; morphine; obsessive-compulsive disorder.  
 XX

OS Mammalia.  
 XX WO200014115-A1.  
 PN  
 XX  
 XX  
 PD 16-MAR-2000.  
 XX  
 XX  
 PF 30-AUG-1999; 99WO-US19790.  
 XX  
 PR 03-SEP-1998; 98US-0099104.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Duman R;  
 PI  
 XX  
 DR WPI; 2000-256944/22.  
 XX  
 XX Identification of compounds that regulate addictive behavior for  
 PT treatment of addictive behavior disorders, such as obsessive-compulsive  
 PT disease, comprises determining whether compounds are antagonists to  
 PT melanocortin-4 receptor -  
 XX  
 PS Claim 1; Fig 1; 62pp; English.  
 XX

CC The invention relates to methods for the identification of compounds  
 CC that regulate addictive behaviour, particularly drug addiction. The  
 CC method comprises determining whether a test compound can bind to and  
 CC antagonise a melanocortin-4 receptor (MC4-R), and administering that  
 CC compound to an animal in order to see if a reduction in addictive  
 CC behaviour occurs. Melanocortins are products of pro-opiomelanocortin  
 CC post-translational processing which are thought to have a broad range of  
 CC physiological actions, including behaviour, learning, memory, analgesia,  
 CC thermoregulation and body weight, as well as their well known effects on  
 CC adrenal cortical functions and on melanocytes. The present invention is  
 CC based on the observations that MC4-R activity potentiates some of the  
 CC addictive effects of drugs of addiction, particularly cocaine and  
 CC morphine, and that knockout mice do not display the behavioural responses  
 CC indicative of addiction caused by chronic and/or acute administration of  
 CC these drugs. The methods are useful for identifying MC4-R inhibitors.  
 CC These compounds may be used to treat addiction to a wide variety of  
 CC substances, including cocaine, opiates, alcohol, hallucinogens, minor  
 CC tranquilisers, nicotine and stimulants. The methods are also useful for  
 CC the treatment of addictive behaviour disorders, including extreme  
 CC craving, addictive psychological disease or obsessive-compulsive  
 CC disorder. The present sequence represents a mammalian MC4-R.  
 XX  
 SQ Sequence 332 AA;

Query Match 93.6%; Score 1617.5; DB 21; Length 332;  
 Best Local Similarity 94.9%; Pred. No. 1.4e-169;  
 Matches 315; Conservative 5; Mismatches 11; Indels 1; Gaps 1;  
 QY 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPFVTLGVISLL 60  
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 2 VNST-HRGHMTSLHLNRRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPFVTLGVISLL 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 ENILVIVATKNNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDQSFVN 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 ENILVIVATKNNKLNHSPMYFFICSLAVADMVLSVNSNGSETIVITLLNSTDQSFVN 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 121 IDNVDSVCSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGGIIICWAACTVS 180  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 121 IDNVDSVCSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGGIIICWAACTVS 180  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTROGAN 240  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 181 GILFIYSDSSAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTROGAN 240  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 241 MKGATLTILIGVFVVCWAPFELHIFVYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 241 HKGATLTILIGVFVVCWAPFELHIFVYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 301 IVALRSQELRKTFFKEIICYPGLGCLDLSRY 332  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 301 IVALRSOELRKTKEIICCYPLGGLCDLSSRY 332

Search completed: June 4, 2003, 18:15:42  
Job time : 53 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 4, 2003, 17:58:11 ; Search time 12.5 seconds  
(without alignments)  
781.473 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGHMTSLHFWNRST.....FKRIICYPGGICDLISRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCRU\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1659.5	96.0	332	1	US-08-671-525B-8
2	1659.5	96.0	332	1	US-08-672-109B-8
3	1659.5	96.0	332	2	US-08-842-045-8
4	1659.5	96.0	332	2	US-08-842-238-8
5	1659.5	96.0	332	2	US-08-780-749A-2
6	1659.5	96.0	332	3	US-08-629-335B-8
7	1659.5	96.0	332	4	US-08-870-511-2
8	1659.5	96.0	332	4	US-09-384-302A-9
9	1653.5	95.7	332	2	US-08-662-560-2
10	1653.5	95.7	332	2	US-08-780-749A-6
11	1653.5	95.7	332	4	US-08-870-511-6
12	1648.5	95.4	332	4	US-08-870-511-8
13	1647.5	95.3	332	4	US-08-870-511-10
14	1647.5	95.3	332	4	US-08-870-511-12
15	1632.5	94.5	332	4	US-09-384-302A-6
16	1613.5	93.4	332	3	US-08-706-281A-16
17	1613.5	93.4	332	4	US-09-097-231-16
18	1407	81.4	293	4	US-09-384-302A-8
19	1030	59.6	325	3	US-08-706-281A-18
20	1030	59.6	325	4	US-09-097-231-18
21	1027	59.4	325	1	US-08-671-525B-10
22	1027	59.4	325	1	US-08-672-109B-10
23	1027	59.4	325	2	US-08-842-045-10
24	1027	59.4	325	2	US-08-842-238-10
25	1027	59.4	325	3	US-08-629-335B-10
26	1004.5	58.1	325	4	US-08-387-805-16
27	987.5	57.1	360	1	US-08-671-525B-6

28	987.5	57.1	360	1	US-08-672-109B-6	Sequence 6, Appli
29	987.5	57.1	360	2	US-08-842-045-6	Sequence 6, Appli
30	987.5	57.1	360	2	US-08-842-238-6	Sequence 6, Appli
31	987.5	57.1	360	2	US-08-780-749A-1	Sequence 1, Appli
32	987.5	57.1	360	3	US-08-629-335B-6	Sequence 6, Appli
33	987.5	57.1	360	4	US-08-870-511-1	Sequence 1, Appli
34	971	56.2	323	2	US-08-044-812A-4	Sequence 4, Appli
35	971	56.2	323	2	US-08-475-637-4	Sequence 4, Appli
36	971	56.2	323	3	US-09-191-359-4	Sequence 4, Appli
37	967	56.0	323	3	US-08-706-281A-12	Sequence 12, Appli
38	967	56.0	323	4	US-09-097-231-12	Sequence 12, Appli
39	754.5	43.7	315	1	US-07-866-979-4	Sequence 4, Appli
40	754.5	43.7	315	2	US-08-466-906B-4	Sequence 4, Appli
41	754.5	43.7	315	3	US-08-706-281A-4	Sequence 4, Appli
42	754.5	43.7	315	4	US-09-201-746-4	Sequence 4, Appli
43	754.5	43.7	315	4	US-09-097-231-4	Sequence 4, Appli
44	752.5	43.5	317	4	US-08-387-805-2	Sequence 2, Appli
45	751.5	43.5	317	1	US-07-866-979-6	Sequence 6, Appli

#### ALIGNMENTS

##### RESULT 1

US-08-671-525B-8  
; Sequence 8, Application US/08671525B  
; Patent No. 5703220  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/671,525B  
; FILING DATE: June 27, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-671-525B-8

Query Match 96.0%; Score 1659.5; DB 1; Length 332;  
Best Local Similarity 96.7%; Pred. No. 1.6e-125;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy	1	MNSTHHGHMTSLHFWNRSTYGHPSNASESLGKGYSDGGCYEQLFVSPVFTLGVISLL	60
Db	2	VNST-HRGMHTSLHFWNRSTYGHPSNASESLGKGYSDGGCYEQLFVSPVFTLGVISLL	60
Qy	61	ENILVIVAIARNKLNHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFTVN	120

Db	61	ENTLVIVATAKNKNLHSPWFFICISLAVADMLVSVNGSETIIITLNLSTDDTDAQFTVN	120
Qy	121	IDNVDSVICSSLLASICSLSIAVDRTFTFYALQYHNIMTVRRVGIIISCIIWAAC	180
Db	121	IDNVDSVICSSLLASICSLSIAVDRTFTFYALQYHNIMTVRRVGIIISCIIWAAC	180
Qy	181	GVLFIIYDSSAVIICLTITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQ	240
Db	181	GILFIIYDSSAVIICLTITMFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQ	240
Qy	241	MKGATLTILIGVYVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLIIMCNSIIDPL	300
Db	241	MKGATLTILIGVYVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLIIMCNSIIDPL	300
Qy	301	IYALRSQELRKTFKEIICCYPLGGCLDSRY	332
Db	301	IYALRSQELRKTFKEIICCYPLGGCLDSRY	332

## RESULT 2

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US-08-672-109B-8
; Sequence 8, Application US/08672109B
; Patent No. 5710265
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672.109B
; FILING DATE: June 27, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-109B-8

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Query Match      96.0%; Score 1659.5; DB 1; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.6e-125;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1

QY      1  MNSTHHGMHTSLHFWNRSTYGPHSNASESLRGKYGSDGCYEQLFVSPPEVFTLGVISLL 60
      :||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      2  VNST-HRCMHTSLHLNWRSSRYLHSNASESLRGKYGSDGCYEQLFVSPPEVFTLGVISLL 60

QY      61  ENILVIVAIAKNKLNHSPMTFFICSLAVADMLVSVSNGSETIVITLLNSTDDAQSFVN 120
      :||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      61  ENILVIVAIAKNKLNHSPMTFFICSLAVADMLVSVSNGSETIIITLLNSTDDAQSFVN 120

QY      121  IDNWDSVICSSLLASTCSLLSTAVDRYFTFYALQYHNIMTVRRVVGIIISCIWAACTVS 180
      :||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||

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Db	121	IDNWIDSVICSLLSASICLSLSIAVDRYFTIFYALQYHNIMTVKRVGIIISCIWAAC	180
Qy	181	GVLFIIYSDSSAVIIICLTITMFTMLALMASLYVHFMARLHKRIAVLPGTGT	240
Db	181	GILFIIYSDSSAVIIICLTITMFTMLALMASLYVHFMARLHKRIAVLPGTG	240
Qy	241	MKGATITLTILIGVFVVCWAPFFLHIFYISCPQNPYCVCFMSHFNL	300
Db	241	MKGATITLTILIGVFVVCWAPFFLHIFYISCPQNPYCVCFMSHFNL	300
Qy	301	IYALRSQELRKTFFKEIICCYPLGGCLDLS	332
Db	301	IYALRSQELRKTFFKEIICCYPLGGCLDLS	332

### RESULT 3

```

RES001 3
US-08-842-045-8
: Sequence 8, Application US/08842045
: Patent No. 5817787
: GENERAL INFORMATION:
: APPLICANT: Yamada, Tadataka
: APPLICANT: Gantz, Ira
: TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
: STREET: P.O. Box 828
: CITY: Bloomfield Hills
: STATE: MI
: COUNTRY: US
: ZIP: 48303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/842,045
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, Deann F.
: REGISTRATION NUMBER: 36683
: REFERENCE/DOCKET NUMBER: 2115-000853DVE
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (810)641-1600
: TELEFAX: (810)641-0270
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 332 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-842-045-8

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	Query Match	96.0%	Score 1659.5	DB 2	Length 332	
	Best Local Similarity	96.7%	Pred. No. 1.6e-125			
	Matches 321	Conservative 5	Mismatches 5	Indels 1	Gaps 1	
Qy	1	MNSTHHGCMTSLHFWNRSTYGP	HNSNASESLGKGYSDGGCYEQ	LFVSPVEVTLGVISLL	60	
Db	2	VNST-HRGMTSLHLWNRSYRL	HNSNASESLGKGYSDGGCYEQ	LFVSPVEVTLGVISLL	60	
Qy	61	ENILVIVIAAKNKLHSPWYFF	ICSLAYADMLVSVNGSETIVITL	NSTDTDAQSFVN	120	
Db	61	ENILVIVIAAKNKLHSPWYFF	ICSLAYADMLVSVNGSETIIITL	NSTDTDAQSFVN	120	
Qy	121	IDNVDSVICSLLASTCSLLST	AVDRYFTIFYALQYHNIMTVR	VGIIISCIWAACPVS	180	
Db	121	IDNVDSVICSLLASTCSLLST	AVDRYFTIFYALQYHNIMTVR	VGIIISCIWAACPVS	180	
Qy	181	GVLFIIYSDSSAVIICITMFF	YMLMALMSLYVHMFMLARKH	KRIAVLPCTGTIQGAN	240	

Db 181 GILFIYSDSAVILICITMFTTLMALMASLYVHMFMLARLHKRIAVLPCTGAIRQAN 240  
Qy 241 MKGAITITILIGVFWCWAPFFHLIFISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAITITILIGVFWCWAPFFHLIFISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCVPLGGLCDLSRY 332  
Db 301 IYALRSQELRKTKEIICCVPLGGLCDLSRY 332

RESULT 4  
US-08-842-238-8  
; Sequence 8, Application US/08842238  
; Patent No. 5869257  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/842.238  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-842-238-8

Query Match 96.08; Score 1659.5; DB 2; Length 332;  
Best Local Similarity 96.7%; Pred. No. 1.6e-125;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MNSHHGMMTSLHFWNKRSTYVPHSNASESLGKGYSDGCGVEQLFVSPVFTLGVISLL 60  
Db 2 VNST-HRGMHTSLHWNRSYRLHNSASESLGKGYSDGCGVEQLFVSPVFTLGVISLL 60  
Qy 61 ENILVIVAIKRNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVAIKRNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Qy 121 IDNVDSVICSLLASCSLLSTAVDRYFTIFALQYHNIMTVRVGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASCSLLSTAVDRYFTIFALQYHNIMTVRVGIIISCIWAACVTS 180  
Qy 181 GVLFIIYSDSAVILICITMFTTLMALMASLYVHMFMLARLHKRIAVLPCTGAIRQAN 240  
Db 181 GILFIYSDSAVILICITMFTTLMALMASLYVHMFMLARLHKRIAVLPCTGAIRQAN 240  
Qy 241 MKGAITITILIGVFWCWAPFFHLIFISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MKGAITITILIGVFWCWAPFFHLIFISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCVPLGGLCDLSRY 332  
Db 301 IYALRSQELRKTKEIICCVPLGGLCDLSRY 332

RESULT 5  
US-08-780-749A-2  
; Sequence 2, Application US/08780749A  
; Patent No. 5932779  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank  
; APPLICANT: Huszar, Dennis  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS  
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/780.749A  
; FILING DATE: 08-JAN-1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Laura A. Coruzzi  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-780-749A-2

Query Match 96.08; Score 1659.5; DB 2; Length 332;  
Best Local Similarity 96.7%; Pred. No. 1.6e-125;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MNSHHGMMTSLHFWNKRSTYVPHSNASESLGKGYSDGCGVEQLFVSPVFTLGVISLL 60  
Db 2 VNST-HRGMHTSLHWNRSYRLHNSASESLGKGYSDGCGVEQLFVSPVFTLGVISLL 60  
Qy 61 ENILVIVAIKRNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVAIKRNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Qy 121 IDNVDSVICSLLASCSLLSTAVDRYFTIFALQYHNIMTVRVGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASCSLLSTAVDRYFTIFALQYHNIMTVRVGIIISCIWAACVTS 180  
Qy 181 GVLFIIYSDSAVILICITMFTTLMALMASLYVHMFMLARLHKRIAVLPCTGAIRQAN 240  
Db 181 GILFIYSDSAVILICITMFTTLMALMASLYVHMFMLARLHKRIAVLPCTGAIRQAN 240  
Qy 241 MKGAITITILIGVFWCWAPFFHLIFISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MKGATLTILIGVVFVVCWAPFFHLHLYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300

QY 301 IVALRSQELRKTFKEIICCYPLGGCLDLSRY 332  
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Db 301 IVALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 6  
US-08-629-335B-8  
; Sequence 8, Application US/08629335B  
; Patent No. 6117975  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/629,335B  
; FILING DATE: July 23, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-629-335B-8

Query Match 96.0%; Score 1659.5; DB 3; Length 332;  
Best Local Similarity 96.7%; Pred. No. 1.6e-125;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGMHTSLHFWNRSTYGPHSNASLSLKGYSDDGCGYBOLFVSPFVTLGVISLL 60  
:|||||

Db 2 VNST-HRGMHTSLHLNRSYRLHNSASLSLKGYSDDGCGYBOLFVSPFVTLGVISLL 60  
:|||||

QY 61 ENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDQSFVTN 120  
:|||||

Db 61 ENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDQSFVTN 120  
:|||||

QY 121 IDNVDSVICSLLASICSLLSIADRVFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180  
:|||||

Db 121 IDNVDSVICSLLASICSLLSIADRVFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180  
:|||||

QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||

Db 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||

QY 241 MKGATLTILIGVVFVVCWAPFFHLHLYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
:|||||

Db 241 MKGATLTILIGVVFVVCWAPFFHLHLYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
:|||||

QY 301 IVALRSQELRKTFKEIICCYPLGGCLDLSRY 332  
|||||

Db 301 IVALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 8  
US-09-384-302A-9  
; Sequence 9, Application US/09384302A  
; Patent No. 6451543  
; GENERAL INFORMATION:  
; APPLICANT: Kochendoerfer, Gerd G  
; APPLICANT: Hunter, Christie L  
; APPLICANT: Kent, Stephen B.H.  
; APPLICANT: Botti, Paolo  
; APPLICANT: Gryphon Sciences  
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis  
; FILE REFERENCE: grfn-028/02WO  
; CURRENT APPLICATION NUMBER: US/09/384,302A  
; CURRENT FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: 09/144,964  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 09/263,971  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 30

Db 301 IVALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 7  
US-08-870-511-2  
; Sequence 2, Application US/08870511  
; Patent No. 6287763  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank  
; APPLICANT: Huszar, Dennis  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE  
; FILE REFERENCE: 7853-083  
; CURRENT APPLICATION NUMBER: US/08/870,511  
; CURRENT FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-870-511-2

Query Match 96.0%; Score 1659.5; DB 4; Length 332;  
Best Local Similarity 96.7%; Pred. No. 1.6e-125;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNSTHHGMHTSLHFWNRSTYGPHSNASLSLKGYSDDGCGYBOLFVSPFVTLGVISLL 60  
:|||||

Db 2 VNST-HRGMHTSLHLNRSYRLHNSASLSLKGYSDDGCGYBOLFVSPFVTLGVISLL 60  
:|||||

QY 61 ENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDQSFVTN 120  
:|||||

Db 61 ENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDQSFVTN 120  
:|||||

QY 121 IDNVDSVICSLLASICSLLSIADRVFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180  
:|||||

Db 121 IDNVDSVICSLLASICSLLSIADRVFTIFVALQYHNIMTVRRVGIISCIWAACVTS 180  
:|||||

QY 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||

Db 181 GVLFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||

QY 241 MKGATLTILIGVVFVVCWAPFFHLHLYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
:|||||

Db 241 MKGATLTILIGVVFVVCWAPFFHLHLYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
:|||||

QY 301 IVALRSQELRKTFKEIICCYPLGGCLDLSRY 332  
|||||

Db 301 IVALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 8  
US-09-384-302A-9  
; Sequence 9, Application US/09384302A  
; Patent No. 6451543  
; GENERAL INFORMATION:  
; APPLICANT: Kochendoerfer, Gerd G  
; APPLICANT: Hunter, Christie L  
; APPLICANT: Kent, Stephen B.H.  
; APPLICANT: Botti, Paolo  
; APPLICANT: Gryphon Sciences  
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis  
; FILE REFERENCE: grfn-028/02WO  
; CURRENT APPLICATION NUMBER: US/09/384,302A  
; CURRENT FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: 09/144,964  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 09/263,971  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 30



; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-384-302A-9

Query Match 96.0%; Score 1659.5; DB 4; Length 332;  
Best Local Similarity 96.7%; Pred. No. 1.6e-125;  
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;  
  
Qy 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Db 2 VNST-HRGMHTSLHLNRRSSYRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60  
  
Qy 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSTVN 120  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Db 61 ENILVIVAIKNNKLNHSPMYFFICSLAVADMLVSVNSGSETIIITLLNSTDTDAQSTVN 120  
  
Qy 121 IDNVDSVICSSLLASCSLLSTAVDRYFTTFYALQYHNMTVRRVGIISCIWAACVTS 180  
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Qy 181 GVLFIIYSDSSAVIICLITMFTMLMASLYVHMFLMARLHKRIAVLPGTGTIROGAN 240  
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Qy 241 MKGAIITLILIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
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Qy 301 IYALRSQELRKTFKEIICCYPLGGLDLSRY 332  
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Db 301 IYALRSQELRKTFKEIICCYPLGGLDLSRY 332

RESULT 9  
US-08-662-560-2  
; Sequence 2, Application US/08662560  
; Patent No. 5908609  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank  
; APPLICANT: Huszar, Dennis  
; APPLICANT: Wei, Gu  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS  
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/662,560  
; FILING DATE: 10-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-060  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-662-560-2

Query Match 95.7%; Score 1653.5; DB 2; Length 332;  
Best Local Similarity 96.4%; Pred. No. 4.7e-125;  
Matches 320; Conservative 5; Mismatches 6; Indels 1; Gaps 1;  
  
Qy 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60  
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Qy 181 GVLFIIYSDSSAVIICLITMFTMLMASLYVHMFLMARLHKRIAVLPGTGTIROGAN 240  
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Db 181 GILFIIYSDSSAVIICLITMFTMLMASLYVHMFLMARLHKRIAVLPGTGTIROGAN 240  
  
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Db 301 IYALRSQELRKTFKEIICCYPLGGLDLSRY 332

RESULT 10  
US-08-780-749A-6  
; Sequence 6, Application US/08780749A  
; Patent No. 5932779  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank  
; APPLICANT: Huszar, Dennis  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS  
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/780,749A  
; FILING DATE: 08-JAN-1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Laura A. Coruzzi  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-064



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: GENERAL INFORMATION:
: APPLICANT: Lee, Frank
: APPLICANT: Huszar, Dennis
: APPLICANT: Gu, Wei
: TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
: TITLE OF INVENTION: REGULATION OF BODY WEIGHT
: FILE REFERENCE: 7853-083
: CURRENT APPLICATION NUMBER: US/08/870,511
: CURRENT FILING DATE: 1997-06-06
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 332
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-870-511-10

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Best Local Similarity 96.1%; Pred. No. 1.4e-124;
Matches 319; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

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QY      241  MKGAITLTILIGVFWVCWAPFFLHLFIYISCPNPYCVCPMSHFNLYLILMCSNIIDPL 300
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QY      301  IYALRSQELRKTFKEIICYPYGLGGLDLSRY 332
Db      301  IYALRSQELRKTFKEIICYPYGLGGLDLSRY 332

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RESULT 14
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; Sequence 12, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITILE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-12

Query Match          95.3%; Score 1647.5; DB 4; Length 332;
Best Local Similarity 96.1%; Pred. No. 1.4e-124;
Matches 319; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 MNSTHHGHMHTSLHFWNRSTYGPHSNASBSLKGYSDDGCYEQLFYSPEVFTLGVISLL 60
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US-09-384-302A-6			
; Sequence 6, Application US/09384302A			
; Patent No. 6451543			
; GENERAL INFORMATION:			
; APPLICANT: Kochendoerfer, Gerd G			
; APPLICANT: Hunter, Christie L			
; APPLICANT: Kent, Stephen B.H.			
; APPLICANT: Botti, Paolo			
; APPLICANT: Gryphon Sciences			
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis			
; TITLE OF INVENTION: Of Membrane Polypeptides			
; FILE REFERENCE: grfn-028/02W0			
; CURRENT APPLICATION NUMBER: US/09/384,302A			
; CURRENT FILING DATE: 1999-08-26			
; PRIOR APPLICATION NUMBER: 09/144,964			
; PRIOR FILING DATE: 1998-08-31			
; PRIOR APPLICATION NUMBER: 09/263,971			
; PRIOR FILING DATE: 1999-03-05			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 6			
; LENGTH: 332			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic			
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Search completed: June 4, 2003, 18:03:56  
Job time : 14 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:01 ; Search time 31 Seconds  
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Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGHTSLHFWNRST.....FKELICYPGLGLDLSSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
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- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1685	97.5	332	9	US-09-884-211A-4
3	1604	92.8	332	9	US-09-910-180-2
4	1004.5	58.1	325	12	US-10-052-545-16
5	1000.5	57.9	323	10	US-09-303-395-2
6	752.5	43.5	317	12	US-10-052-545-2
7	721	41.7	297	9	US-10-151-431-4
8	711	41.1	296	12	US-10-015-948-2
9	697	40.3	297	9	US-10-151-431-6
10	356.5	20.6	364	9	US-09-971-228-6
11	356.5	20.6	364	9	US-09-811-838-2
12	356.5	20.6	364	10	US-09-842-316-3
13	356.5	20.6	364	10	US-09-731-030A-15
14	356.5	20.6	364	12	US-10-037-616-20
15	328	19.0	104	12	US-10-052-545-10
16	327	18.9	102	12	US-10-052-545-8
17	325	18.8	382	10	US-09-969-711-2
18	324.5	18.8	381	9	US-10-024-494-28
19	324.5	18.8	381	10	US-09-827-937A-18

20	324.5	18.8	381	10	US-09-842-316-6	Sequence 6, Appli
21	324.5	18.8	381	10	US-09-731-030A-17	Sequence 17, Appl
22	324	18.8	341	9	US-09-971-228-13	Sequence 13, Appl
23	324	18.8	346	9	US-09-971-228-15	Sequence 15, Appl
24	324	18.8	362	10	US-09-993-844-8	Sequence 8, Appli
25	324	18.8	381	12	US-10-037-616-19	Sequence 19, Appl
26	324	18.8	382	9	US-09-971-228-5	Sequence 5, Appli
27	324	18.8	382	9	US-09-759-514-2	Sequence 2, Appli
28	316.5	18.3	330	10	US-09-845-720-2	Sequence 2, Appli
29	314.5	18.2	353	9	US-09-971-228-11	Sequence 11, Appl
30	314.5	18.2	353	9	US-09-811-838-6	Sequence 6, Appli
31	314.5	18.2	353	9	US-10-097-340-338	Sequence 338, App
32	314.5	18.2	353	10	US-09-842-316-4	Sequence 4, Appli
33	314.5	18.2	353	10	US-09-731-030A-16	Sequence 16, Appl
34	314.5	18.2	353	12	US-10-037-616-25	Sequence 25, Appl
35	312.5	18.1	321	9	US-10-146-065-2	Sequence 2, Appli
36	308.5	17.9	348	10	US-09-903-799-2	Sequence 2, Appli
37	305.5	17.7	354	10	US-09-879-225-2	Sequence 2, Appli
38	304.5	17.6	353	10	US-09-771-063-2	Sequence 2, Appli
39	304.5	17.6	353	10	US-09-771-063-4	Sequence 4, Appli
40	304.5	17.6	353	12	US-10-037-616-23	Sequence 23, Appl
41	304	17.6	352	9	US-10-084-507B-21	Sequence 21, Appl
42	303.5	17.6	124	12	US-10-052-545-12	Sequence 12, Appl
43	303.5	17.6	353	9	US-10-084-507B-22	Sequence 22, Appl
44	303.5	17.6	353	10	US-09-731-030A-19	Sequence 19, Appl
45	302.5	17.5	330	10	US-09-845-720-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
US-09-884-211a-3  
; Sequence 3, Application US/09884211a  
; Publication No. US20030032791A1  
; GENERAL INFORMATION:  
; APPLICANT: Alan et. al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: PCL0743A  
; CURRENT APPLICATION NUMBER: US/09/884, 211a  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Feline MC4R protein Sequence  
US-09-884-211a-3

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Best Local Similarity	100.0%	Pred. No.	9.3e+148;				
Matches	332;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MNSTHHGHTSLHFWNRSTYGP	HNASESLGKGYSDGGCYEQLFVSP	EVFTLGVISLL	60		
Qy	61	ENILVIVAIAKNNLHSPMYFFIC	SLAVADMLVSNVSGSETIVITLLNST	DTDAQSFVN	120		
Db	61	ENILVIVAIAKNNLHSPMYFFIC	SLAVADMLVSNVSGSETIVITLLNST	DTDAQSFVN	120		
Qy	121	IDNVDSYICSSLLASICSLSIAV	DRYFTTFYALQYHNIMTVRRVGI	IIISCIWAACFVS	180		
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## RESULT 2

US-09-884-211A-4  
; Sequence 4, Application US/09884211A  
; Publication No. US20030032791A1  
; GENERAL INFORMATION:  
; APPLICANT: Alan et. al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: PC10743A  
; CURRENT APPLICATION NUMBER: US/09/884,211A  
; PRIOR FILING DATE: 2000-06-26  
; PRIOR FILING DATE: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Canine MC4R protein Sequence  
US-09-884-211A-4

Query Match 97.5%; Score 1685; DB 9; Length 332;  
Best Local Similarity 97.6%; Pred. No. 6.9e-144;  
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Db 61 ENILVIVATAKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
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QY 301 IYALRSQELRKTKEIICCPYLGGLDLSRY 332  
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## RESULT 3

US-09-910-180-2  
; Sequence 2, Application US/09910180  
; Publication No. US20030082678A1  
; GENERAL INFORMATION:  
; APPLICANT: Hsiung, Hansen  
; APPLICANT: Smith, Dennis  
; APPLICANT: Zhang, Xing-Yue  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING BODY WEIGHT IN BOVINE SPECIES  
; FILE REFERENCE: P-12621  
; CURRENT APPLICATION NUMBER: US/09/910,180  
; CURRENT FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Bovine  
US-09-910-180-2  
Query Match 92.8%; Score 1604; DB 9; Length 332;  
Best Local Similarity 94.3%; Pred. No. 1.4e-136;  
Matches 313; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
QY 1 MNSTHHGMHTSLHFNWNRSTYGPHSNASSESLGKGYSDGCGYEQLFVSPFVTLGVISLL 60  
|||||  
Db 1 MNSTPLGHTSLHFNWNRSAHGMPNTVSESLAKGYSDGCGYEQLFVSPFVTLGVISLL 60  
QY 61 ENILVIVATAKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVATAKNNLHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVICSSLLASICSLLSIADVDYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASICSLLSIADVDYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180  
QY 181 GVLFIYSDSSAVIICLIITMFTMLMASLVYHMFMLARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GVLFIYSDSSAVIICLIITMFTMLMASLVYHMFMLARLHKRIAVLPGTGTIRQGAN 240  
QY 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
Db 241 MKGATITLILGVVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
QY 301 IYALRSQELRKTKEIICCPYLGGLDLSRY 332  
Db 301 IYALRSQELRKTKEIICCPYLGGLDLSRY 332

## RESULT 4

US-10-052-545-16  
; Sequence 16, Application US/10052545  
; Patent No. US20020142392A1  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/052,545  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,805  
; FILING DATE: 21-FEB-95  
; APPLICATION NUMBER: PCT/DK93/00273  
; FILING DATE: 20-AUG-93  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1046/92  
; FILING DATE: 21-AUG-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1118/92  
; FILING DATE: 10-SEP-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0528/93

; FILING DATE: 05-MAY-93  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cimbala, Michele A.  
 ; REGISTRATION NUMBER: 33,851  
 ; REFERENCE/DOCKET NUMBER: 1102.0160000  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 371-2600  
 ; TELEFAX: (202) 371-2540  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 325 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-10-052-545-16

Query Match 58.1%; Score 1004.5; DB 12; Length 325;  
 Best Local Similarity 61.1%; Pred. No. 1.2e-82;  
 Matches 203; Conservative 44; Mismatches 76; Indels 9; Gaps 4;  
 QY 1 MNSTHHGCHTSLHFWNRSTYGHPSNASESLGKGYSDGGCYEQLFVSPVEVFTLGVISLL 60  
 DB 1 MNSSEH-----LHFLDLNLNATEGNLSGPNVKNKS-SPC-EDMGIAVEVFTLGVISLL 52  
 QY 61 ENILVIVAIAKNKLNHSPMYFFICGLAVADMLVSVNGSETIVITLLNSTD-TDAQSFV 119  
 DB 53 ENILVIGAIVKKNKLNHSPMYFFVCSLAVADMLVSMSSAWETITVLLNKKHLVIADAFVR 112  
 QY 120 NIDNVIDVSCSLASTCSLLSIADRYFTIFVALQVHNMTVRRVGGIISCIWAACV 179  
 DB 113 HIDNVFDSMICSIVVASCSSLAIAVDYVTFVALRVHMTARRSGAIIAGIWAFCG 172  
 QY 180 SGVFLIYSDSSAVTICITLFTFMALMASLYVHMFMLKRIKRIAVLPCTGTIROGA 239  
 DB 173 CGVFLIYSESTYVILCLISFFFAFLVLLVSLYHMFLLATHVKRIALCPGALRGPR 232  
 QY 240 NKGAITLITLIGVGVVCAWPFLLHFIYISCPQNPYCVCFMSHFNLYLILIMCNSIDP 299  
 DB 233 AWQAVVTMLLGVFTVCWAPFLLHLLTLMSCPNLYCSRFMSHFNLYLILIMCNSVMDP 292  
 QY 300 LIYALRSOELKRTKEIKCCVPLGLGLDLSSR 331  
 DB 293 LIYAFRSOEMRKRTKEIKCCRCGRFIACSPRR 324

RESULT 5  
 ; US-09-903-395-2  
 ; Sequence 2, Application US/09903395  
 ; Patent No. US20020068324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Allen, Keith D.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING  
 ; FILE REFERENCE: R-653  
 ; CURRENT APPLICATION NUMBER: US/09/903,395  
 ; PRIOR FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: US 60/218,074  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/243,958  
 ; PRIOR FILING DATE: 2000-10-26  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 323  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-903-395-2

Query Match 57.9%; Score 1000.5; DB 10; Length 323;  
 Best Local Similarity 61.9%; Pred. No. 2.8e-82;  
 Matches 185; Conservative 50; Mismatches 53; Indels 11; Gaps 3;  
 QY 23 PHSNASESLGKGYSDGGCYEQLFVSPVEVFTLGVISLLENILVIVAIAKNKLNHSPMYFF 82

Db 25 PASNRSGS-----GFCEQVFKPEVELALGIVLSMLNITLVILAVVRNGLNLSHPMYFF 76  
 QY 83 ICSLAVADMLVSVNGSETIVITLLNSTD-TDAQSFVHNIDNVIDSDVSCSLASICSLL 141  
 DB 77 LCSLAAADMLVSLNSLETIMIAVINDSLTLEQFTOHMDNIFDSMICISLVASICNLL 136  
 QY 142 SIADRYFTIFVALQVHNMTVRRVGGIISCIWAACVSGVLFIIYSDSSAVIICLTIMF 201  
 DB 137 AIAIDRYVTIFVALRVHSIMTVRKALFLIGVWCCGICGVWFIIYSEKMWIVCLTIMF 196  
 QY 202 FTMLALMASLYVHMFMLKRIKRIAVLPCTGTI--RQANMKGAITLITLIGVGVVCA 259  
 DB 197 FAMVLLMGTLYHMFLEFARLHVQRIAVLPAGVAPQOQSHCMKGAVTITLLGVIFCWA 256  
 QY 260 PFFLHLFIYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSOELKRTKEIK 318  
 DB 257 PFFLHLVLIITCPTNPYCYTAHFTVLYLIMCNSVIDPLIYAFRSLELRNTKREILC 315

RESULT 6  
 ; US-10-052-545-2  
 ; Sequence 2, Application US/10052545  
 ; Patent No. US20020142392A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Steirne, Kessler, Goldstein & Fox  
 ; STREET: 1100 New York Ave., N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/052,545  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/387,805  
 ; FILING DATE: 21-FEB-95  
 ; APPLICATION NUMBER: PCT/DK93/00273  
 ; FILING DATE: 20-AUG-93  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DK 1046/92  
 ; FILING DATE: 21-AUG-92  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DK 1118/92  
 ; FILING DATE: 10-SEP-92  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DK 0528/93  
 ; FILING DATE: 05-MAY-93  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cimbala, Michele A.  
 ; REGISTRATION NUMBER: 33,851  
 ; REFERENCE/DOCKET NUMBER: 1102.0160000  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 371-2600  
 ; TELEFAX: (202) 371-2540  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 317 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: polypeptide  
 ; US-10-052-545-2

```
Query Match      43.5%; Score 752.5; DB 12; Length 317;
Best Local Similarity 51.2%; Pred. No. 5.7e-60;
Matches 152; Conservative 51; Mismatches 89; Indels 5; Gaps 4;

QY 27 ASSESLGKGYSDGG--CYEQLFVSPEVFTLVGLVLSLENIIVIVAIKNNKLNHSPMYFFIC 84
Db 20 AIPOLGLAANQTCARCLE-VISDGLFLSLGLSVLENALVWATIAKNNRNHSPMYCFIC 78
QY 85 SLAVADMLVSVNGSETIVITLLNSTDTDAQSFTV-NIDNVDSVICSSLLASICSLSIA 143
Db 79 CLALSDLLVSGSVNLETAVILLLEAGALVARAAVLOQLDNVIDVITCSSMSSLCFLGAI 138
QY 144 ADVRYTIFVALQYHNIMTVRRVGGIIISCIWAACVSGVLFIYSDSSAVIICLIMFTT 203
Db 139 ADVRYISIFVALYHSIVTLPRARRRVAALVWASVVFTLFIAYDHVAVLLCLVVFELA 198
QY 204 MLALMASLYVHMFELMARLHKRTAVL-PGTGTTIROGANKMGATITLILGVFVVCWAPFF 262
Db 199 MLVLMVAVLYVHMLARACQAQIARLHKRQRPVHOGFGLKGAVTLTILIGIFLCLWGPF 258
QY 263 LHLIFYISCPNPYCVCFMSHFNLYLILMCNSIIDPLIYALRSOELRKTFRKEIICC 319
Db 259 LHLTLVLCPEHEHTCCICFNFNFLLALICNAIIDPLIYAFHSOELRRTLKEVLTC 315

RESULT 7
US-10-151-431-4
; Sequence 4, Application US/10151431
; Publication No. US20030044973A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Mountjoy, Kathleen G
; TITLE OF INVENTION: Mammalian Adrenocorticotrophic Hormone
; Receptors and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allegrretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/151,431
; FILING DATE: 20-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,298
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/866,560
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030044973A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-151-431-4

Query Match      41.7%; Score 721; DB 9; Length 297;
Best Local Similarity 46.1%; Pred. No. 3.6e-57;
Matches 142; Conservative 58; Mismatches 90; Indels 18; Gaps 3;

QY 26 NASESLGKGYSDGGCYEQLFVSPEVFTLVGLVLSLENIIVIVAIKNNKLNHSPMYFFICS 85
Db 6 NSYENINNTARNNSDCPRVLPPEEIPFTTISVGLVENLIVLLAVFKNKNLQAPMYFFICS 65
QY 86 LAVADMLVSVNGSETIVITLLNSTDTDAQ-SFTVNIDNVDSVICSSLLASICSLSIA 144
Db 66 LAISDMLGSLYKILENILLILRNMGYLKPRGSFETADDDIISLVSILGSIFFSLVIA 125
QY 145 VDRYTFIFVALQYHNIMTVRRVGGIIISCIWAACVSGVLFIYSDSSAVIICLIMFTT 204
Db 126 ADRYITIFHALRYHSIVTMRRTVWLTVITWCTGTGTTWIFSHHVPVITFTSLFPLM 185
QY 205 LALMASLYVHMFELMARLHKRTAVLPGTGTIROGANKMGATITLILGVFVVCWAPFFLH 264
Db 186 LVFILCLYVHMFELMARSHTRKISTLP-----RANMKGAITLTILLGVIFCWAPFVLH 238
QY 265 LIFYISCPNPYCVCFMSHFNLYLILMCNSIIDPLIYALRSOELRKTFRKEIICCYPG 324
Db 239 VILMTFCPSNPYCAVMSLFQVNGMLMCNAVIDPIYAFRSPDELDAFKKMFIC----- 293
QY 325 LCDLSSRY 332
Db 294 -----SRY 296

RESULT 8
US-10-015-948-2
; Sequence 2, Application US/10015948
; Patent No. US20020133843A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
; ADRENOCORTICOTROPIN HORMONE RECEPTOR GENE DISRUPTIONS
; FILE REFERENCE: R-605
; CURRENT APPLICATION NUMBER: US/10/015,948
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,906
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/324,583
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-015-948-2

Query Match      41.1%; Score 711; DB 12; Length 296;
Best Local Similarity 50.7%; Pred. No. 2.9e-56;
Matches 138; Conservative 47; Mismatches 79; Indels 8; Gaps 2;

QY 49 EVFVTLVGLVLSLENIIVIVAIKNNKLNHSPMYFFICTSLAVADMLVSVNGSETIVITLLN 108
Db 29 EIFFTISVIGILENIVLLAVIKNNLQSPMYFFICTSLAISDMLGSLYKILENIMTFERN 88
QY 109 STDTDAQ-SFTVNIDNVDSVICSSLLASICSLSIAVDVRYTIFVALQYHNIMTVRRVG 167
Db 89 MGYLPRGSFETADDDIIDCMFILSLGSIFFSLVIAADRYITIFHALQYHSIVTMRRTI 148
QY 168 ITISCIWAACVSGVLFIYSDSSAVIICLIMFTTLMALMASLYVHMFELMARLHKRTIA 227
Db 149 ITLTIWMEFCGSGITWIFSHHITVLTFTSLFLLMLVFIILCLYIHNELLARSHARKIS 208
QY 228 VLPGTGTIROGANKMGATITLILGVFVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLY 287
Db 209 TLPR-----NMKGAMTLTILLGVIFCWAPFVLHVLMLTFCPNPNPYCVCMISLQVFN 261
```







Db 189 ICDIENSNAPLYSDSYLFWAIFNL--VTFVVMVLYAHIFGYVRQRTMRMS-RHSSG 245  
Qy 234 TIROGANNKGA1-TLTILIGVVFVVCWAPFELHLIFLYSCQNPYCV-C-FMSHFNLYLILI 291  
Db 246 PRNRDTMMSLLKTVVILGAFICWTPGLVLLDLDVCCPQ-----CDVLAVERFFULLA 300  
Qy 292 MCNSIIDPLIYALRSQBLRTFKBIICC 319  
Db 301 EFNSAMNPIIYVRDKEMSATFRQILCC 328

## RESULT 14

US-10-037-616-20  
; Sequence 20, Application US/10037616  
; Patent No. US20020123148A1  
; GENERAL INFORMATION:  
; APPLICANT: English, Denis  
; APPLICANT: Kovacs, Richard J.  
; APPLICANT: Rizzo, Maria T.  
; APPLICANT: Silva, Daniel T.  
; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use  
; FILE REFERENCE: 7042-119  
; CURRENT APPLICATION NUMBER: US/10/037,616  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/243,887  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-616-20

Query Match 20.6%; Score 356.5; DB 12; Length 364;  
Best Local Similarity 28.4%; Pred. No. 3e-24;  
Matches 93; Conservative 65; Mismatches 115; Indels 55; Gaps 11;  
Qy 15 FWRSTYGPHS---NASESIGKGYSDGCGYEQLFVSPEVFTLGVLSLENTILVIVVIA 70  
Db 33 FYNKS--GKHLATEWNTVSKLVMLG-----ITVCIFIMLANLLVMVVIY 75  
Qy 71 KKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDSTAQSFTVINDVIDSVIC 130  
Db 76 VNRFEHPPIYLYMANLAADFFAGLA-----YFIMFNTGPNTRRLTVSTWLLRQGLID 129  
Qy 131 SSLASTCSLLSTAVDRYFTFYVALQYHNIMTVRRVGGIISCIWAACVTSVGV----- 182  
Db 130 TSLTASVANLATAIERHITVF-RMQLHTRMSNRVWVVIWITMAIVMGATPSVGVWNC 188  
Qy 183 -----LFYISDSSAVTICLTMTFFTMALMASLYVHMFMLARLHKRIAVLPCTG 233  
Db 189 ICDIENSNAPLYSDSYLFWAIFNL--VTFVVMVLYAHIFGYVRQRTMRMS-RHSSG 245  
Qy 234 TIROGANNKGA1-TLTILIGVVFVVCWAPFELHLIFLYSCQNPYCV-C-FMSHFNLYLILI 291  
Db 246 PRNRDTMMSLLKTVVILGAFICWTPGLVLLDLDVCCPQ-----CDVLAVERFFULLA 300  
Qy 292 MCNSIIDPLIYALRSQBLRTFKBIICC 319  
Db 301 EFNSAMNPIIYVRDKEMSATFRQILCC 328

## RESULT 15

US-10-052-545-10  
; Sequence 10, Application US/10052545  
; Patent No. US20020142392A1  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/052,545  
; FILING DATE:

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,805  
; FILING DATE: 21-FEB-95  
; APPLICATION NUMBER: PCT/DK93/00273  
; FILING DATE: 20-AUG-93  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1046/92;  
; FILING DATE: 21-AUG-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1118/92;  
; FILING DATE: 10-SEP-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0528/93;  
; FILING DATE: 05-MAY-93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1102.0160000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 104 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
US-10-052-545-10

Query Match 19.0%; Score 328; DB 12; Length 104;  
Best Local Similarity 60.6%; Pred. No. 2.5e-22;  
Matches 63; Conservative 17; Mismatches 22; Indels 2; Gaps 1;

Qy 152 FYALQYHNIMTVRRVGGIISCIWAACVTSVGVLFYISDSSAVIICLTITMFFMLMASL 211  
Db 1 FYALRYHSIVTVRRALTLIVAIWCCVGVVFYISDKMWIVCLITMFFAMLLMGLT 60  
Qy 212 YVHMFMLARLHKRIAVLPCTGT--RQGANMKGAITLTILIGV 253  
Db 61 YVHMFLEPRLHVRKRIALPPADGVAPQOHSCKMGAVTLLIGI 104

Search completed: June 4, 2003, 18:13:53  
Job time : 32 secs

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241 MKGAI TLTILIGVFVVCWAPFFLHLIFYISCPONPYCVCFM SHFNLYLILMCNSIIDPL 300

Db 241 MKGATITLTILIGVYVWCPFFLHLFIYISCPQNPVCVCFMSHFNLILIMCNSIDPL 300  
|||||

QY 301 IVALRSQELRKTKFKETICCPYLGGLDLSRY 332  
|||||

Db 301 IVALRSQELRKTKFKETICCPYLGGLDLSRY 332  
|||||

## RESULT 2

B57055 melanocortin-4 receptor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-Oct-1995 #sequence\_revision 02-Jul-1996 #text\_change 07-May-1999

C:Accession: B57055

R:Mountjoy, K.G.; Moutrid, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.

Mol. Endocrinol. 8, 1298-1308, 1994

A:Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and autonomic nervous system

A:Reference number: A57055; MUID:95157557; PMID:7854347

A:Accession: B57055

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-215 <MUD>

C:Superfamily: melanocortin receptor

Query Match 62.2%; Score 1074; DB 2; Length 215;

Best Local Similarity 97.2%; Pred. No. 1.4e-80;

Matches 209; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 78 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSFNTNIDNIDSVICSSLLASI 137  
|||||

Db 1 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSFNTNIDNIDSVICSSLLASI 60  
|||||

QY 138 CSLLSIAVDRYFTIFALQYHNMVRRVGGIISCIWAACVSGVLFIIYDSSSAVIICL 197  
|||||

Db 61 CSLLSIAVDRYFTIFALQYHNMVRRVGGIISCIWAACVSGVLFIIYDSSSAVIICL 120  
|||||

QY 198 ITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVC 257  
|||||

Db 121 ITMFFTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVC 180  
|||||

QY 258 WAPFELHLFIYISCPQNPVCVCFMSHFNLILIM 292  
|||||

Db 181 WAPFELHLFIYISCPQNPVCVCFMSHFNLILIM 215  
|||||

## RESULT 3

JC2193

melanocortin receptor, MC5 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 24-Sep-1999

C:Accession: JC2193

R:Griffon, N.; Mignon, V.; Facchinetti, P.; Diaz, J.; Schwartz, J.C.; Sokoloff, P.

Biochem. Biophys. Res. Commun. 200, 1007-1014, 1994

A:Title: Molecular cloning and characterization of the rat fifth melanocortin receptor.

A:Reference number: JC2193; MUID:94234987; PMID:8179577

A:Accession: JC2193

A:Molecule type: DNA

A:Residues: 1-325 <GRI>

A:Cross-references: GB:L27081; NID:9435606; PIDN:AAA41577.1; PID:9435607

C:Superfamily: melanocortin receptor

C:Keywords: G protein-coupled receptor; receptor; transmembrane protein

F:37-63/Domain: transmembrane #status predicted <TM1>

F:73-98/Domain: transmembrane #status predicted <TM2>

F:117-138/Domain: transmembrane #status predicted <TM3>

F:159-179/Domain: transmembrane #status predicted <TM4>

F:193-211/Domain: transmembrane #status predicted <TM5>

F:240-263/Domain: transmembrane #status predicted <TM6>

F:276-297/Domain: transmembrane #status predicted <TM7>

Query Match

Best Local Similarity 60.6%; Score 1047; DB 2; Length 325;

Matches 202; Conservative 46; Mismatches 59; Indels 4; Gaps 3;

QY 26 NASES--LGKGYSD--GGCYEQLFVSPVFTLGVISLLENILVIVAIAKNKNLHSPMYFF 82  
|||||

Db 15 NASEDNILQNNYNNKSSACEDMGIAVEVFLTLGLVSLLENILVIGAIKKNLHSPMYFF 74  
|||||

QY 83 ICSLAVADMLVSVNGSETIVITLLNSTD--TDAQSFNTNIDNIDSVICSSLLASTCSLL 141  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 75 VGS LAVADMLVSVNGSETIVITLLNSTD--TDAQSFNTNIDNIDSVICSSLLASTCSLL 134  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 142 STAVDRYFTIFALQYHNMVRRVGGIISCIWAACVSGVLFIIYDSSSAVIICLTIMF 201  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 135 ATAVDRYFTIFALQYHNMVRRVGGIISCIWAACVSGVLFIIYDSSSAVIICLTIMF 194  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 202 FTMLALMASLYVHMFMLARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPF 261  
|||||

Db 195 FTMLFMVSLYIHMFLARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPF 254  
|||||

QY 262 FTMLFMVSLYIHMFLARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPF 321  
|||||

Db 255 FTMLFMVSLYIHMFLARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPF 314  
|||||

QY 322 LGGLCDLSRY 332  
|||||

Db 315 FRRTCTLLGRY 325  
|||||

## RESULT 4

I49008

melanocortin-5 receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Sep-1999

C:Accession: I49008; A54245; JC2244

R:Pathi, Z.; Iben, L.G.; Parker, E.M.

Neurochem. Res. 20, 107-113, 1995

A:Title: Cloning, expression, and tissue distribution of a fifth melanocortin receptor

A:Reference number: I49008; MUID:95258173; PMID:7739752

A:Accession: I49008

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-372 <RES>

A:Cross-references: EMBL:U08354; NID:9522165; PIDN:AAA76585.1; PID:9522166

R:Labbe, O.; Desarnaud, F.; Eggerickx, D.; Vassart, G.; Parmentier, M.

Biochemistry 33, 4543-4549, 1994

A:Title: Molecular cloning of a mouse melanocortin 5 receptor gene widely expressed

A:Reference number: A54245; MUID:94213827; PMID:8161509

A:Accession: A54245

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 48-120, F', 122-372 <LAB>

A:Cross-references: GB:X76295; NID:9498973; PIDN:CAA53943.1; PID:9498974

A:Experimental source: clone HGMP01B

A:Note: sequence extracted from NCBI backbone (NCBIP:145988)

R:Gantz, I.; Shimoto, Y.; Konda, Y.; Miwa, H.; Dickinson, C.J.; Yamada, T.

Biochem. Biophys. Res. Commun. 200, 1214-1220, 1994

A:Title: Molecular cloning, expression, and characterization of a fifth melanocortin

A:Reference number: JC2244; MUID:94241974; PMID:8185570

A:Accession: JC2244

A:Molecule type: DNA

A:Residues: 48-372 <GAN>

A:Cross-references: GB:L22527; NID:9468377; PIDN:AAA21337.1; PID:9468378

C:Comment: This protein responds to melanocortins with an increase in intracellular c

C:Superfamily: melanocortin receptor

C:Keywords: receptor; transmembrane protein

F:84-109/Domain: transmembrane #status predicted <TM1>

F:121-144/Domain: transmembrane #status predicted <TM2>

F:164-185/Domain: transmembrane #status predicted <TM3>

F:206-226/Domain: transmembrane #status predicted <TM4>

F:232-257/Domain: transmembrane #status predicted <TM5>

F:287-310/Domain: transmembrane #status predicted <TM6>

F:324-344/Domain: transmembrane #status predicted <TM7>

Query Match

Best Local Similarity 59.4%; Score 1027; DB 2; Length 372;

Matches 199; Conservative 46; Mismatches 62; Indels 4; Gaps 3;

```
QY 26 NASES--LGKGYSDG-CYEQLFVSPEVFTLGVISLLENILVIVAIKNNLHSPMYFF 82
    |||  ||  :  |||:|||||:|||||  ||  |||:|||||:
Db 62 NASEDGLGSNVNKNKLACEEMGIAVEVFTLGLVSLLENILVIVAIKNNLHSPMYFY 121
QY 83 ICSLAVADMLVSVNGSESTIVITLLNSTD-TDAOSFTVNIIDVSDVSCSLLASICSLL 141
    :|||||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 122 VGS LAVADMLVSMNAWETVIYLLNNKHLVIADTFVRHIDNVFDSMICSIVVASMCSLL 181
QY 142 SIADVRFITFYALQYHNIMTVRRVGIISCIWAACVTSGVLFIYSDSSAVIICLTIMF 201
    :|||||  |||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 182 AIADVRYTITFYALRYHHIMTARRSGVLIACIWFICSGVFIYIYESKVIICLISMF 241
QY 202 FTMLALMASLVYHMFMLARLHKRIAVLPGTGTIRQGANMKGAITLTLLIGVFVVCWAPF 261
    |||  |||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 242 FTMLFFVSVLYIHMFLARNHVKRIASPRNSYRQRTSMKGAITLTMLLIGFIVCNSPF 301
QY 262 FLHLFIYISCPQNPYCVCFMNFHNLILIMCNSIIDPLIYALRSQELRKTFKEIICYP 321
    |||  |||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 302 FLHLILMISCPQNPYCVCFMNFYNNYLLILIMCNSVIDPLIYALRSQEMRRTFKEIVCCHG 361
QY 322 LGGCLDLSRY 332
    |  |  |
Db 362 FRPRLGGY 372
```

```
RESULT 5
JC5592
melanocortin 5 receptor - human
C:Species: Homo sapiens (man)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 07-May-1999
C:Accession: JC5592
R:Fraendberg, P.A.; Xu, X.; Chhajlani, V.
Biochem. Biophys. Res. Commun. 236, 489-492, 1997
A:Title: Glutamine-235 and arginine-272 in human melanocortin 5 receptor determines its
A:Reference number: JC5592; MUID:97382462; PMID:9240466
A:Accession: JC5592
A:Molecule type: protein
A:Residues: 1-325 <FR2>
C:Comment: This protein is the melanocortin receptor with low affinity towards alpha-MSH
F:37-61/Domain: transmembrane #status predicted <TM1>
F:77-100/Domain: transmembrane #status predicted <TM2>
F:115-138/Domain: transmembrane #status predicted <TM3>
F:156-179/Domain: transmembrane #status predicted <TM4>
F:187-210/Domain: transmembrane #status predicted <TM5>
F:240-263/Domain: transmembrane #status predicted <TM6>
F:274-297/Domain: transmembrane #status predicted <TM7>
```

```
Query Match 59.2%; Score 1023.5; DB 2; Length 325;
Best Local Similarity 62.0%; Pred. No. 2.9e-76;
Matches 206; Conservative 43; Mismatches 74; Indels 9; Gaps 4;
QY 1 MNSTHHGMHTSLHFNWSTYGPNSASESLGKGYSDGCVQLFVSPEVFTLGVISLL 60
    |||  |||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 1 MNSSFH-----LHFLDLNLNATEGNLSPNVKNKS-SPC-EDMGIAVEVFTLGVISLL 52
QY 61 ENILVIVAIKNNLHSPMYFFICSLAVADMLVSVNGSESTIVITLLNSTD-TDAQSTFV 119
    |||  |||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 53 ENILVIGAVKNNLHSPMYFFVCSLAVADMLVSMSSAWETITVLLNNKHLVIADAFVR 112
QY 120 NIDNVDSVICSSLLASICSLLSIADVRYTFYALQYHNIMTVRRVGIISCIWAACVT 179
    :||||  |||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 113 HIDNVDSMICISVVASCSLLAIAVDYVTFYALRYHHIMTARRSGAIIAGIWAFTG 172
QY 180 SGVLFIYSDSSAVIICLTIMFTMLALMASLVYHMFMLARLHKRIAVLPGTGTIROGA 239
    :||||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 173 CGIVFIYSESTYVILCLISIMFFAMFLVLSLYIHMFLARLTHVKRIALCPGALRGSRP 232
QY 240 NMKGAITLTLLIGVFVVCWAPFFLHLFIYISCPQNPYCVCFMNFHNLILIMCNSIIDP 299
    :||||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 233 SMOGAVTVMLLGVFTVCWAPFFLHLTLMLSCPNLYCSRFMSHFNFYLLILIMCNSVMDP 292
```

```
QY 300 LIYALRSQELRKTFKEIICCYPLGCLDLSR 331
    |||  |||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 293 LIYAYRSQEMRKTFKEIICCRGFIACSFPRR 324
```

```
RESULT 6
JN0764
melanocortin receptor 2 - human
C:Species: Homo sapiens (man)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 17-Mar-1999
C:Accession: JN0764; S37042; S40681
R:Chhajlani, V.; Muceniece, R.; Wikberg, J.E.S.
Biochem. Biophys. Res. Commun. 195, 866-873, 1993
A:Title: Molecular cloning of a novel human melanocortin receptor.
A:Reference number: S40681; MUID:93384614; PMID:8396929
A:Accession: JN0764
A:Molecule type: DNA
A:Residues: 1-325 <CH>
A:Cross-references: EMBL:225470
A:Experimental source: brain
C:Superfamily: melanocortin receptor
C:Keywords: glycoprotein; receptor; transmembrane protein
F:38-61/Domain: transmembrane #status predicted <TM1>
F:74-97/Domain: transmembrane #status predicted <TM2>
F:115-138/Domain: transmembrane #status predicted <TM3>
F:156-179/Domain: transmembrane #status predicted <TM4>
F:187-211/Domain: transmembrane #status predicted <TM5>
F:240-265/Domain: transmembrane #status predicted <TM6>
F:274-297/Domain: transmembrane #status predicted <TM7>
F:274,20,28/Binding site: carbohydrate (Asn) #status predicted
```

```
Query Match 58.1%; Score 1004.5; DB 2; Length 325;
Best Local Similarity 61.1%; Pred. No. 1e-74;
Matches 203; Conservative 44; Mismatches 76; Indels 9; Gaps 4;
QY 1 MNSTHHGMHTSLHFNWSTYGPNSASESLGKGYSDGCVQLFVSPEVFTLGVISLL 60
    |||  |||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 1 MNSSFH-----LHFLDLNLNATEGNLSPNVKNKS-SPC-EDMGIAVEVFTLGVISLL 52
QY 61 ENILVIVAIKNNLHSPMYFFICSLAVADMLVSVNGSESTIVITLLNSTD-TDAQSTFV 119
    |||  |||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 53 ENILVIGAVKNNLHSPMYFFVCSLAVADMLVSMSSAWETITVLLNNKHLVIADAFVR 112
QY 120 NIDNVDSVICSSLLASICSLLSIADVRYTFYALQYHNIMTVRRVGIISCIWAACVT 179
    :||||  |||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 113 HIDNVDSMICISVVASCSLLAIAVDYVTFYALRYHHIMTARRSGAIIAGIWAFTG 172
QY 180 SGVLFIYSDSSAVIICLTIMFTMLALMASLVYHMFMLARLHKRIAVLPGTGTIROGA 239
    :||||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 173 CGIVFIYSESTYVILCLISIMFFAMFLVLSLYIHMFLARLTHVKRIALCPGALRGSRP 232
QY 240 NMKGAITLTLLIGVFVVCWAPFFLHLFIYISCPQNPYCVCFMNFHNLILIMCNSIIDP 299
    :||||:|||||:|||||:|||||:|||||  ||  |||:|||||:
Db 233 AMOGAVTVMLLGVFTVCWAPFFLHLTLMLSCPNLYCSRFMSHFNFYLLILIMCNSVMDP 292
QY 300 LIYALRSQELRKTFKEIICCYPLGCLDLSR 331
    |||  |||:|||||:|||||  ||  |||:|||||:|||||  ||  |||:|||||:
Db 293 LIYAFRSQEMRKTFKEIICCRGFIACSFPRR 324
```

```
RESULT 7
S43850
melanocortin 3 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 24-Sep-1999
C:Accession: S43850; S37153
R:Desarnaud, F.; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.
Biochem. J. 299, 367-373, 1994
A:Title: Molecular cloning, functional expression and pharmacological characterization
A:Reference number: S43850; MUID:94226597; PMID:8172596
A:Accession: S43850
A>Status: preliminary
A:Molecule type: DNA
```

Query Match	57.5%;	Score	993.5;	DB	2;	Length	360;
Best Local Similarity	62.0%;	pred.	No. 9e-74;				
Matches	186;	Conservative	49;	Mismatches	58;	Indels	7;
Gaps	3;						
QY	26	NASESLGKGY	----	SDGGCEYQLEFVSP	FTVTGLVTSLL	ENILVIVAI	AKNNLHSPMYF
DB	53	NGSEHLQAPFFS	NOSSAFCEQVKEP	ELSLGIVSLL	ENILVILAVVR	GNLHSPMYF	112
QY	82	FTCSLAVADMVLSV	NSGETIVITL	NSTD-TDAQSFT	VNIDNVDSV	ICSSLLASICSL	140
DB	113	FLCSLAVADMVLSV	NSALETIMAI	THSDDYTFEDQ	FIQHMDFID	MTCISLVA	SICNL 172
QY	141	LSIAVDRYFTIFYALQ	YHNTVRRVGIIS	CTWAACTVSGV	LFIIYDSSA	VITCLITM	200
DB	173	LAIADVRTTIFYALR	VHSMTVRKALT	LIVLWCCGCGV	GVFIYSESKM	VIVCLITM	232
QY	201	FFTMLALMASLYV	HMFMLARHLK	RIKRAVLPGTGI	--RQGANMK	GAITITILIGV	FFVVCW 258
DB	233	FFAMMLMGTLV	VHMFELFARL	HKRIAALPPADG	VAPQOHSCKM	GAIVITILIGV	FIETW 292
QY	259	APFELHLIFYIS	CPQNPYCVCF	WSHFNLYLIL	IMCNSIID	PLIYALR	SOELRKTFKEIC 318
DB	293	APFELHLVLIIT	CTNPCTCYTAH	FTYLVLMCM	NSVIDPLI	YAFRSLEL	RNTRFELIC 352

QY	26	NASESLGKGY----	SDGCGYEOLFVSPVEVFTVLGVLISLENILVIVAIKNNKLSHPMWF	81
Db	53	NGSEHLQAPFFSNGOSSAFCEQVFIKEPFLSGIVSSLENILVILVUAVVNGNLSPMWF	112	
QY	82	FTCSLAVADMVLVSNGSETIVITLLNSTD-TDAQSFTVNDINVDIVSCSLLASICSL	140	
Db	113	FLCSLAVADMVLVSNALETIMIAIVHSDDYTFEDQFIQHMDNIFDSMICISILVASICNL	172	
QY	141	LSIADVDRFTTFYALQVYHNIMTVRRVCGIIISCITWAACACTVSGVLFIYSDSSAVITCLITM	200	
Db	173	LAIADVDRVITTFYALRYHSTMTVRKALTLLVAILWCCGCVGVFIYVSESKNIVICLITM	232	
QY	201	FFTMLALMASLYVHMFMLARHLKRIAVLPCTGTI--ROGANNKMGAITLITILIGVFVVCW	258	
Db	233	FFAMLLMGTLVYHMFLEARLHVKRTAALPPADGVAPQOHSCKMGNAVITILIGVFICW	292	
QY	259	APFFLHLFIYISCPQNPYCVCFWSHFNLYLILIMCNSIIDPLIYALRSGOEUKTKFEIC	318	
Db	293	APFFLHLVLIITCTPNPCYCYAHFTNYLVLMCMNSVIDPLIYAFRSLRNTPREILC	352	

Query Match 55.9%; Score 965.5; DB 2; Length 325;  
Best Local Similarity 59.2%; Pred. NO. 1.6e-71;





A:Molecule type: DNA  
A:Residues: 1-317 <VAG>  
A:Cross-references: GB:571017; NID:g547325; PIDN:AAB31361.1; PID:g547326  
C:Superfamily: melanocortin receptor

Query Match 44.8%; Score 773.5; DB 2; Length 317;  
Best Local Similarity 50.7%; Pred. No. 7.4e-56;  
Matches 153; Conservative 54; Mismatches 82; Indels 13; Gaps 3;

QY 20 TYGPHSNASBSLGKSGDGCYQQLFVSPFVTLGVISLLENILVIAIAKKNLHSPM 79  
DB 25 TLAPNRTPGQCLEVSSLDG-----LFLSLGLSVLENVVLVAAIAKKNLHSPM 73  
QY 80 YFFICSLAVADMVLVSVNGSETIVITLLNSTDTDAQFTV-NIDNVIDSVICSSLLASIC 138  
DB 74 YFFICCLAVSDLLVSVNLETAVMPLLEAGVLATQAAVQQLDNVIDLVICGSMVSSLC 133  
QY 139 SLLSIAVDRYFTIFYALQVHNMTVRRVGIISCIWAACVTSGVLFIYSDSSAVIICLI 198  
DB 134 FLGAIAVDRIYSIFYALRVHSVTLPRAMRIIAIIVASILTSLFFITYNHRKVLCLV 193  
QY 199 TMEFTMLAMSLVYHMFMLARHIKRIAVL-PGTGTIRQGANMKGAITLTILIGVFVVC 257  
DB 194 GLFIAMALMAVLYVHMLARACQHARGIARLQKRPRIHQGFLGKAATLTILIGVFVFC 253  
QY 258 WAPFFLHLIFYISCPONPYCVCFMSHFNLYLILMNCNSIIDPLIYALRSQELRKTKKEII 317  
DB 254 WGPFFLHLILVLCPOHPTCGCTGCFKFNFLALIIICNAIVDPLIYAFRSQELRKTLQEV 313  
QY 318 CC 319  
DB 314 QC 315

RESULT 14  
T12055  
melanocyte stimulating hormone receptor - red fox  
C:Species: Vulpes vulpes (red fox)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: T12055  
R:Vage, D.I.; Lu, D.; Klungland, J.; Lien, S.; Adalsteinsson, S.; Cone, R.D.  
Nature Genet. 15, 311-315, 1997  
A:Title: A non-epistatic interaction of agouti and extension in the fox, Vulpes vulpes.  
A:Reference number: 217397; MUID:97207656; PMID:9054949  
A:Accession: T12055  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-317 <VAG>  
A:Cross-references: EMBL:X90844; NID:g1781363; PIDN:CAA62349.1; PID:g1806567  
C:Genetics:  
A:Gene: MC1-R  
C:Superfamily: melanocortin receptor  
C:Keywords: hormone receptor

Query Match 44.2%; Score 763; DB 2; Length 317;  
Best Local Similarity 53.7%; Pred. No. 5.4e-55;  
Matches 146; Conservative 54; Mismatches 70; Indels 2; Gaps 2;

QY 50 VFVTLGVISLLENILVIAIAKKNLHSPMVFICSLAVADMVLVSVNGSETIVITLLNS 109  
DB 44 LFLSLGLSVLENVVLVAAIAKKNLHSPMVFICGLAVSDLLVSVTNVLETAVMLLVEA 103  
QY 110 TDTAQSFV-NIDNVIDSVICSSLLASICSLISIAVDRYFTIFYALQVHNMTVRRVGI 168  
DB 104 GALAAQAAVVQQLDDIIDVLICGSMVSSLCFLGATAVDRLSIFYALRVHSIVTLPRWR 163  
QY 169 IISCIWAACVTSGVLFIYSDSSAVIICLTMEFTMLAMSLVYHMFMLARHIKRIAV 228  
DB 164 AISAIWVASVLSSTLFIATYNHTAVLLCLVSPFVAMLVMLVYHMLARARQHARGIAR 223  
QY 229 L-PGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPONPYCVCFMSHFNLY 287  
DB 224 LAKRQHSVHQGFLGKAATLTILIGVFVVCWGPFFLHLILVLCPOHPTCGCTGCFKFNFL 283

QY 288 LILIMCNSIIDPLIYALRSQELRKTKKEIICC 319  
DB 284 LTLIICNSIIDPFIYAFRSQELRKTLQEVVLC 315

RESULT 15  
S25581  
melanocyte-stimulating hormone receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Oct-1999  
C:Accession: S25581; A43265  
R:Mountjoy, K.G.; Robbins, L.S.; Mortrud, M.; Cone, R.D.  
submitted to the EMBL Data Library, April 1992  
A:Description: Cloning of a family of genes encoding the melanocortin receptors.  
A:Reference number: S25557  
A:Accession: S25581  
A:Molecule type: mRNA  
A:Residues: 1-315 <MOU>  
A:Cross-references: EMBL:X65635; NID:g53244; PIDN:CAA46589.1; PID:g53245  
R:Mountjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Cone, R.D.  
Science 257, 1248-1251, 1992  
A:Title: The cloning of a family of genes that encode the melanocortin receptors.  
A:Reference number: A43265; MUID:92390715; PMID:1325670  
A:Accession: A43265  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-10 'V', 12-187 'I', 189-315 <MO2>  
A:Experimental source: Cloudman S91 melanoma cell line  
A:Note: sequence extracted from NCBI backbone (NCBIP:112486)  
C:Superfamily: melanocortin receptor  
C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 43.7%; Score 754.5; DB 2; Length 315;  
Best Local Similarity 50.7%; Pred. No. 2.6e-54;  
Matches 153; Conservative 59; Mismatches 81; Indels 9; Gaps 6;

QY 24 HSNASESLG--KGYSDGCGYEQLFVS-PE-VFVTLGVISLLENILVIAIAKKNLHSPM 79  
DB 15 NSNATSHLGLATNQSEPCW---LYVSIPTDGLFSLGLSVLENVVLVIAITKKNLHSPM 71  
QY 80 YFFICSLAVADMVLVSVNGSETIVITLLNSTDTDAQ-SFTVNTDNVIDSVICSSLLASIC 138  
DB 72 YFFICCLAVSDLLVSVNLETTIILLEVGLVARVALVQQLDNVIDLVICGSMVSSLC 131  
QY 139 SLLSIAVDRYFTIFYALQVHNMTVRRVGIISCIWAACVTSGVLFIYSDSSAVIICLI 198  
DB 132 FLGIADRIYSIFYALRVHSIVTLPRARRAVGVIMVSVISSTLTITYKKHTAVLLCLV 191  
QY 199 TMEFTMLAMSLVYHMFMLARHIKRIAVL-PGTGTIRQGANMKGAITLTILIGVFVVC 257  
DB 192 TFFLAMALMAITLYAHMETRACQHVQGIQLHKRRSIRQGCFLKGAATLTILIGVFVLC 251  
QY 258 WAPFFLHLIFYISCPONPYCVCFMSHFNLYLILMNCNSIIDPLIYALRSQELRKTKKEII 317  
DB 252 WGPFFLHLILVLCPOHPTCGCTGCFKFNFLIIVLSSTVDPLIYAFRSQELRKTLQEV 311  
QY 318 CC 319  
DB 312 LC 313

Search completed: June 4, 2003, 18:19:07  
Job time: 27 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 18:04:01 ; Search time 14 seconds  
(without alignments)  
983.581 Million cell updates/sec

Title: US-09-884-211a-3

Perfect score: 1728

Sequence: 1 MNSTHHGHMTSLHFNWNRST.....FKREIIICYPGLGICDLSSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1698	98.3	332	1	MC4R_PIG
2	1659.5	96.0	332	1	MC4R_HUMAN
3	1652	95.6	332	1	MC4R_RAT
4	1604	92.8	332	1	MC4R_BOVIN
5	1047	60.6	325	1	MC5R_RAT
6	1030.5	59.6	325	1	MC5R_PANTR
7	1030	59.6	325	1	MC5R_MOUSE
8	1026.5	59.4	325	1	MC5R_HUMAN
9	1000.5	57.9	323	1	MC3R_MOUSE
10	988.5	57.2	360	1	MC3R_HUMAN
11	972.5	56.3	325	1	MC5R_BOVIN
12	971	56.2	323	1	MC3R_RAT
13	965.5	55.9	325	1	MC5R_SHEEP
14	939	54.3	294	1	MC5R_PIG
15	932	53.9	184	1	MC4R_MOUSE
16	819.5	47.4	314	1	MSHR_CHICK
17	777.5	45.0	317	1	MSHR_CAPCA
18	777.5	45.0	317	1	MSHR_DANDA
19	775.5	44.9	317	1	MSHR_BOVIN
20	773.5	44.8	317	1	MSHR_ALCAA
21	767.5	44.4	317	1	MSHR_CAPHI
22	767.5	44.4	317	1	MSHR_SHEEP
23	765.5	44.3	317	1	MSHR_CEREL
24	765.5	44.3	317	1	MSHR_OVIMO
25	765	44.3	317	1	MSHR_RANTA
26	763	44.2	317	1	MSHR_CANFA
27	763	44.2	317	1	MSHR_VULVU
28	760.5	44.0	283	1	MSHR_PIG
29	754.5	43.7	315	1	MSHR_MOUSE
30	754.5	43.7	317	1	MSHR_HUMAN
31	750.5	43.4	317	1	MSHR_PANTR
32	733.5	42.4	292	1	MSHR_HORSE
33	721	41.7	297	1	ACTR_HUMAN

34 718 41.6 295 1 ACTR\_SHEEP  
35 717 41.5 297 1 ACTR\_BOVIN  
36 711 41.1 296 1 ACTR\_MOUSE  
37 709 41.0 297 1 ACTR\_MESAU  
38 684 39.6 297 1 ACTR\_CAVPO  
39 361 20.9 364 1 EDG2\_MOUSE  
40 356.5 20.6 364 1 EDG2\_HUMAN  
41 354 20.5 393 1 EDG2\_SHEEP  
42 351 20.3 364 1 EDG2\_BOVIN  
43 341.5 19.8 334 1 GP12\_HUMAN  
44 331.5 19.2 334 1 GP12\_RAT  
45 328.5 19.0 383 1 EDG1\_RAT

## ALIGNMENTS

## RESULT 1

MC4R\_PIG  
ID MC4R\_PIG STANDARD; PRT; 332 AA.  
AC O97504: Q9N274; Q9N141;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanocortin-4 receptor (MC4-R).  
GN MC4R.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPRAIN-LND; TISSUE-Kidney;  
RA Ito Y., Minezawa M.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 73-320 FROM N.A., AND VARIANT ASN-298.  
RX MEDLINE=20122164; PubMed=10656927;  
RA Kim K.S., Larsen N., Short T., Plastow G., Rothschild M.F.;  
RT "A missense variant of the porcine melanocortin-4 receptor (MC4R) gene is associated with fatness, growth, and feed intake traits.";  
RL Mamm. Genome 11:131-135(2000).  
RP SEQUENCE OF 75-142 FROM N.A.  
RC TISSUE-Hypothalamus;  
RA Matteri R.L., Dyer C.J.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.  
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE CYCLASE (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; AB021664; BAA36170.1; -  
DR EMBL; AF087937; AAF31753.1; -  
DR EMBL; AF227727; AAF34778.1; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHDOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_FL1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEPTOR\_FL2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Phosphorylation; Lipoprotein; Palmitate; Polymorphism.  
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 106 2 (POTENTIAL).
FT DOMAIN 107 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 145 3 (POTENTIAL).
FT DOMAIN 146 165 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 166 186 4 (POTENTIAL).
FT DOMAIN 187 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 215 5 (POTENTIAL).
FT DOMAIN 216 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 271 6 (POTENTIAL).
FT DOMAIN 272 280 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 281 304 7 (POTENTIAL).
FT DOMAIN 305 332 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 318 318 PALMITATE (POTENTIAL).
FT VARIANT 298 D -> N (ASSOCIATED WITH LESS BACKFAT
THICKNESS, SLOWER GROWTH RATE AND LOWER
FEED INTAKE).
SQ SEQUENCE 332 AA; 36946 MW; 5CD1CD67008BFC81 CRC64;
Query Match 98.3%; Score 1698; DB 1; Length 332;
Best Local Similarity 98.2%; Pred. No. 3.8e-105;
Matches 326; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 MNSTHHGHTSLHFWNRSTYGHNSASESLGKGYSDGGCYQLFVSPFVTLGVISLL 60
Db 1 MNSTHHGHTSLHFWNRSTYGHNSASEPLGKGYSEGCGYQLFVSPFVTLGVISLL 60
QY 61 ENILVITAKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db 61 ENILVITAKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
QY 121 INVIDSVCSLLASICSLLSTAVDRYETIYALQYHNMVRRVGVIIISCIWAACVTS 180
Db 121 INVIDSVCSLLASICSLLSTAVDRYETIYALQYHNMVRRVGVIIISCIWAACVTS 180
QY 181 GVLIIFYSDSSAVIICLIITMFTMLMALASLVHMFMLARHLHKRIAVLPGTGTIROGAN 240
Db 181 GVLIIFYSDSSAVIICLIITVFTMLMALASLVHMFMLARHLHKRIAVLPGTGTIROGAN 240
QY 241 MKGATLTLLIGVYVVCWAPFELHLIFITSCPNPCVCFMSHENLYLILMCNLSIIDPL 300
Db 241 MKGATLTLLIGVYVVCWAPFELHLIFITSCPNPCVCFMSHENLYLILMCNLSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
RESULT 2
MC4R_HUMAN STANDARD; PRT; 332 AA.
AC F32245; Q16317;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanocortin-4 receptor (MC4-R).
GN MC4R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93315499; PubMed=8392067;
RA Gantz I., Miwa H., Konda Y., Shimoto Y., Tashiro T., Waston S.J.,
RA Delvalle J.;
RT "Molecular cloning, expression, and gene localization of a fourth
melanocortin receptor.";
RL J. Biol. Chem. 268:15174-15179(1993).
```

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RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=95157557; PubMed=7854347;
RA Mountjoy K.G., Mortrud M.T., Low M.J., Simerly R.B., Cone R.D.;
RT "Localization of the melanocortin-4 receptor (MC4-R) in
neuroendocrine and autonomic control circuits in the brain.";
RL Mol. Endocrinol. 8:1298-1308(1994).
RN [3]
RP VARIANTS.
RX MEDLINE=99213892; PubMed=10199800;
RA Hinney A., Schmidt A., Nottelboom K., Heibult O., Becker I., Ziegler A.,
RA Gerber G., Sina M., Gorg T., Mayer H., Siegfried W., Fichter M.,
RA Remschmidt H., Hebebrand J.;
RT "Several mutations in the melanocortin-4 receptor gene including a
nonsense and a frameshift mutation associated with dominantly
inherited obesity in humans.";
RL J. Clin. Endocrinol. Metab. 84:1483-1486(1999).
CC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, PLACENTAL, AND GUT TISSUES.
CC -1- DISEASE: DEFECTS IN MC4R SEEM TO PLAY A ROLE IN THE GENETIC
PREDISPOSITION TO OBESITY.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
CC -----
DR EMBL; L08603; AAA35791.1; -.
DR EMBL; S77415; AAB33341.1; -.
DR PIR; A47111; A47111.
DR Genew; HGNC:6932; MC4R.
DR MIM; 155541; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PROSITE; PS00437; G-PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate; Polymorphism;
KW Disease mutation; Obesity.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 106 2 (POTENTIAL).
FT DOMAIN 107 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 145 3 (POTENTIAL).
FT DOMAIN 146 165 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 166 186 4 (POTENTIAL).
FT DOMAIN 187 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 215 5 (POTENTIAL).
FT DOMAIN 216 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 271 6 (POTENTIAL).
FT DOMAIN 272 280 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 281 304 7 (POTENTIAL).
FT DOMAIN 305 332 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 318 318 PALMITATE (POTENTIAL).
FT VARIANT 30 30 S -> R (IN OBESITY).
FT VARIANT 37 37 D -> V (IN OBESITY).
FT VARIANT 78 78 P -> L (IN OBESITY).
FT VARIANT 103 103 /FTID=VAR_010706.
FT VARIANT 103 103 I -> V.
```

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FT VARIANT 112 112 /FTid=VAR_010707.
FT T -> M (IN OBESITY).
FT /FTid=VAR_010708.
FT VARIANT 165 165 R -> W (IN OBESITY).
FT /FTid=VAR_010709.
FT VARIANT 251 251 I -> L.
FT /FTid=VAR_010710.
FT VARIANT 252 252 G -> S (IN OBESITY).
FT /FTid=VAR_010711.
FT VARIANT 317 317 I -> T (IN OBESITY).
FT /FTid=VAR_010712.
FT CONFLICT 169 169 I -> S (IN REF. 2).
FT SEQUENCE 332 AA; 36956 MW; 1C89752CF4DF30C CRC64;

Query Match 96.0%; Score 1659.5; DB 1; Length 332;
Best Local Similarity 96.7%; Pred. No. 1.3e-102;
Matches 321; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2 VNST-HRGMTSLHLNRRSSRLHNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60

Qy 61 ENILVIVIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 ENILVIVIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

Qy 121 IDNVDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 IDNVDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 121 IDNVDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 IDNVDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 181 GVLFIIYSDSSAVIICLITMFTMLMALMASLYVHMFMLMARLHKRIAVLPCTGTIROGAN 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 GILFIIYSDSSAVIICLITMFTMLMALMASLYVHMFMLMARLHKRIAVLPCTGTIROGAN 240

Qy 241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300

Qy 301 IYALRSQELRKTKEIICCPYLGGLDLSRY 332
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 IYALRSQELRKTKEIICCPYLGGLDLSRY 332

RESULT 3
MC4R_RAT ID MC4R_RAT STANDARD; PRT; 332 AA.
AC P70596;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
GN Melanocortin-4 receptor (MC4-R).
OS MC4R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96387362; PubMed=8794897;
RA Alvaro J.D., Tatro J.B., Quillan J.M., Fogliano M., Eisenhard M.,
RA Lerner M.R., Nestler E.J., Duman R.S.;
RT "Morphine down-regulates melanocortin-4 receptor expression in brain
RT regions that mediate opiate addiction.";
RL Mol. Pharmacol. 50:583-591(1996).
CC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
CC ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, ENRICHED IN THE STRIATUM, NUCLEUS
CC ACCUMBENS, AND PERIAQUE-DUCTAL GRAY.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U67863; AAB36517.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECF1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 106 2 (POTENTIAL).
FT DOMAIN 107 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 145 3 (POTENTIAL).
FT DOMAIN 146 165 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 166 186 4 (POTENTIAL).
FT DOMAIN 187 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 215 5 (POTENTIAL).
FT DOMAIN 216 248 6 (POTENTIAL).
FT TRANSMEM 249 271 7 (POTENTIAL).
FT DOMAIN 272 280 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 281 304 7 (POTENTIAL).
FT DOMAIN 305 332 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 318 318 PALMITATE (POTENTIAL).
SQ SEQUENCE 332 AA; 36986 MW; E0E9BAC7E7D168E6 CRC64;

Query Match 95.6%; Score 1652; DB 1; Length 332;
Best Local Similarity 95.2%; Pred. No. 4.1e-102;
Matches 316; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MNSTHHGHTSLHFWNRSTYGPNSNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MNSTHHGHTSLHFWNRSSHLGNASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60

Qy 61 ENILVIVIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 ENILVIVIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

Qy 121 IDNVDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 IDNVDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 181 GVLFIIYSDSSAVIICLITMFTMLMALMASLYVHMFMLMARLHKRIAVLPCTGTIROGAN 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 GVLFIIYSDSSAVIICLITMFTMLMALMASLYVHMFMLMARLHKRIAVLPCTGTIROGAN 240

Qy 241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
241 MKGAITITLIGVFWVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILMCSNIDPL 300

Qy 301 IYALRSQELRKTKEIICCPYLGGLDLSRY 332
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 IYALRSQELRKTKEIICFPYLGGLDLPGRY 332

RESULT 4
MC4R_BOVIN ID MC4R_BOVIN STANDARD; PRT; 332 AA.
AC Q9GLJ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```





30-MAY-2000 (Rel. 39, Last annotation update)  
 Melanocortin-5 receptor (MC5-R).  
 MC5R.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=129/SV;  
 MEDLINE=94213827; PubMed=8161509;  
 Labbe O., Desarnaud F., Egerickx D., Vassart G., Parmentier M.;  
 "Molecular cloning of a mouse melanocortin 5 receptor gene widely  
 expressed in peripheral tissues.";  
 Biochemistry 33:4543-4549(1994).  
 [2]  
 SEQUENCE FROM N.A.  
 MEDLINE=94241974; PubMed=8185570;  
 Gantz I., Shimoto Y., Konda Y., Miwa H., Dickinson C.J., Yamada T.;  
 "Molecular cloning, expression, and characterization of a fifth  
 melanocortin receptor.";  
 Biochem. Biophys. Res. Commun. 200:1214-1220(1994).  
 [3]  
 SEQUENCE FROM N.A.  
 TISSUE=Brain;  
 MEDLINE=95258173; PubMed=7739752;  
 Fathi Z., Iben L.G., Parker E.M.;  
 "Cloning, expression, and tissue distribution of a fifth melanocortin  
 receptor subtype.";  
 Neurochem. Res. 20:107-113(1995).  
 CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE  
 ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE  
 IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: SKIN, ADRENAL GLAND, SKELETAL MUSCLE,  
 BONE MARROW, SPLEEN, THYMUS, GONADS, UTERUS AND BRAIN  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 -----  
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 -----  
 EMBL: X76295; CAAS3943.1; -  
 EMBL: L22527; AAA21337.1; -  
 EMBL: U08354; AAA76585.1; ALT\_INIT.  
 PIR: A54245; A54245.  
 MGD: MGI:99420; Mc5r.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 37  
 FT 1 37 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 38 61 1 (POTENTIAL).  
 FT DOMAIN 62 73  
 FT 62 73 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 74 97 2 (POTENTIAL).  
 FT DOMAIN 98 114  
 FT 98 114 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 115 138 3 (POTENTIAL).  
 FT DOMAIN 139 155  
 FT 139 155 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 156 179 4 (POTENTIAL).  
 FT DOMAIN 180 186  
 FT 180 186 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 187 211 5 (POTENTIAL).  
 FT DOMAIN 212 239  
 FT 212 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 265 6 (POTENTIAL).  
 FT DOMAIN 266 273  
 FT 266 273 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 274 297 7 (POTENTIAL).  
 FT DOMAIN 298 325  
 FT 298 325 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 2  
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 311 311 PALMITATE (POTENTIAL).  
 FT LIPID 312 312 PALMITATE (POTENTIAL).  
 FT CONFLICT 74 74 F -> Y (IN REF. 2 AND 3).  
 SQ SEQUENCE 325 AA; 36953 MW; 5A014D1C1E0157EE CRC64;  
 Query Match 59.68; Score 1030; DB 1; Length 325;  
 Best Local Similarity 64.38; Pred. No. 3.1e-61;  
 Matches 200; Conservative 45; Mismatches 62; Indels 4; Gaps 3;  
 Qy 26 NASES--LGKGYSDG-CYEOLFSPVFTLGVISLLENLIVATAKNKLNHSPMYFF 82  
 Db 15 NASEDGLGSNVKNKSLACEEMGIAVEFLTLGLVSLLENLIVGAIVKNKLNHSPMYFF 74  
 Qy 83 ICSLAVADMLVSVNGSETIVITLLNSTD-TDAQSFVNIDNVDSVCSLLASICSL 141  
 Db 75 VGSILAVADMLVSVNSNAWETVITLLNKNHLVIAIDTFVRHIDNVFDSMCSLL 134  
 Qy 142 SIAVDYFTIFALQYHNIMTVRVGIIISCIWAACVSGVLFIYISDSSAVIICLTMP 201  
 Db 135 AIAVDYITIFALRVHHIMTARRSGVIAIACIWFSCGIVFIYIYESKYVILISMF 194  
 Qy 202 FTMLALMASLVHMLARHLRIKRIAVLPCTGTIRQGANMKGAITLILIGVVCWAPF 261  
 Db 195 FTMLFFVSLYIHMELARHNRKRIASPRYSVRQRTSMKGATLTLMLGIFIVCSPP 254  
 Qy 262 FLHLIFVISCQPNQYCVCFMSHNLXLYLILIMCNSIIDPLIYALRSQELRTFKIICYP 321  
 Db 255 FLHLIIMISCPNQYCVCFMSHNLXLYLILIMCNSIIDPLIYALRSQELRTFKIICYP 314  
 Qy 322 LGGLCDLSRY 332  
 Db 315 FRPRCLLGGY 325

## RESULT 8

MC5R\_HUMAN  
 ID MC5R\_HUMAN STANDARD; PRT; 325 AA.  
 AC P33032;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Melanocortin-5 receptor (MC5-R) (MC-2).  
 GN MC5R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=93384614; PubMed=8396929;  
 RA Chhajlani V., Muceniec R., Wikberg J.E.S.;  
 RT "Molecular cloning of a novel human melanocortin receptor.";  
 RL Biochem. Biophys. Res. Commun. 195:866-873(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94234987; PubMed=8179577;  
 RA Griffon N., Mignon V., Facchinetti P., Diaz J., Schwartz J.C.,  
 RA Sokoloff P.;  
 RT "Molecular cloning and characterization of the rat fifth melanocortin  
 receptor.";  
 RL Biochem. Biophys. Res. Commun. 200:1007-1014(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=95258173; PubMed=7739752;  
 RA Fathi Z., Iben L.G., Parker E.M.;  
 RT "Cloning, expression, and tissue distribution of a fifth melanocortin  
 receptor subtype.";



```
RL Neurochem. Res. 20:107-113(1995).
RN [4]
RP VARIANT LEU-209.
RX MEDLINE=21184529; PubMed=11286624;
RA Hata N., Dixon C., Ray A.J., Phillips S.R., Cunliffe W.J., Dale M.,
RA Todd C., Meggit S., Birch-Wachin M.A., Rees J.L.;
RT "Expression, candidate gene, and population studies of the
RT melanocortin 5 receptor."
RL J. Invest. Dermatol. 116:564-570(2001).
CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: IS EXPRESSED IN THE BRAIN BUT NOT IN THE
CC MELANOMA CELLS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; Z25470; CAA80962.1; -.
DR EMBL; L27080; AAA59566.1; -.
DR EMBL; U08353; AAB60376.1; -.
DR Genew; HGNC:6933; MC3R.
DR MIM; 600042; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
KW Phosphorylation; Lipoprotein; Palmitate; Polymorphism.
FT DOMAIN 1 37
FT TRANSMEM 38 61
FT DOMAIN 62 73
FT TRANSMEM 74 97
FT DOMAIN 98 114
FT TRANSMEM 115 135
FT DOMAIN 139 155
FT TRANSMEM 156 179
FT DOMAIN 180 186
FT TRANSMEM 187 211
FT DOMAIN 212 239
FT TRANSMEM 240 265
FT DOMAIN 266 273
FT TRANSMEM 274 297
FT DOMAIN 298 325
FT CARBOHYD 2 2
FT CARBOHYD 15 15
FT CARBOHYD 20 20
FT CARBOHYD 28 28
FT LIPID 311 311
FT LIPID 312 312
FT VARIANT 209 209
FT CONFLICT 149 149
FT CONFLICT 221 234
FT CONFLICT 297 297
FT SEQUENCE 325 AA; 36600 MW; 8BEC17E1BDAU59BB CRC64;
Query Match 59.4%; Score 1026.5; DB 1; Length 325;
Best Local Similarity 62.0%; Pred. No. 5.2e-61;
Matches 206; Conservative 44; Mismatches 73; Indels 9; Gaps 4;
Qy 1 MNSTHHGHGHTSLHFHNKSTVPHNSASESLGKGYSDGGCVQELFVSEVFTLGVISLL 60
Db 1 MNSSFH-----LHFLDLNLNATEGLNLSGPNVKNKS-SPC-EDMGIAVEVFTLGVISLL 52
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QY 61 ENILVIVAIKAKNKLHSPMYFFICSLAVADMVLVSNVSGSETIVITILLSTD-TDAQSFV 119
Db 53 ENILVIGAIKVNKNLHSPMYFVCSLAVADMVLVSNSSAWETITIVLLNNKHLVIADAFVR 112
QY 120 NIDNVIDSVCSLLASLCSLLSIAVDYFTFYALQYHNMVRRVGIISCIWAACTV 179
Db 113 HDNVFDSMIGTISVVASMSLLAIAVDYFTFYALRYHHIMTARRSGAIIAGIAFCVG 172
QY 180 SCVFLIYSDSSAVIICLTMTFFTMLMASLYVHFMELMARLHRIKRIAVLPGTGTROGA 239
Db 173 CGIVFILYSESYVILCLISMFFAMFLVLLSVLIHMFLLARLTHVRKRIALPGASSARQRT 232
QY 240 NMKGAITLITLIGVFVWCWAPFFLHLIFVISPQNPYCVCFMSHENLYLLIMCNSIIDP 299
Db 233 SMOGAVTYMLLGVFTVCWAPFFLHLMSCPNLYCSRFSHFNMYLLIMCNSVMDP 292
QY 300 LIYALRSQELRRTFKELIICVPLGGLCDLSSR 331
Db 293 LIYAFRSQEMRKTKEIICCRGFRIACSFPR 324
RESULT 9
MC3R_MOUSE STANDARD; PRT; 323 AA.
ID MC3R_MOUSE AC P33033;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Melanocortin-3 receptor (MC3-R).
OS MC3R.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94226597; PubMed=8172596;
RA Desarnaud F., Labbe O., Eggerickx D., Vassart G., Parmentier M.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of a mouse melanocortin receptor gene.";
RL Biochem. J. 299:367-373(1994).
CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X74983; CAA52918.1; -.
DR PIR; S37153; S37153.
DR MGD; MGI:96929; MC3R.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 37
FT TRANSMEM 38 63
FT DOMAIN 64 75
FT TRANSMEM 76 100
FT DOMAIN 101 118
FT TRANSMEM 119 140
FT DOMAIN 141 160
FT CYTOPLASMIC (POTENTIAL).
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FT TRANSMEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 210 5 (POTENTIAL).
FT DOMAIN 211 245 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 268 6 (POTENTIAL).
FT DOMAIN 269 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 323 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 315 315 PALMITATE (POTENTIAL).
SQ SEQUENCE 323 AA; 35806 MW; F4B7B02FAA87B7B CRC64;

Query Match 57.9%; Score 1000.5; DB 1; Length 323;
Best Local Similarity 61.9%; Pred. No. 2.7e-59;
Matches 185; Conservative 50; Mismatches 53; Indels 11; Gaps 3;

QY 23 PHNASESLGKGYSDGGCEYQFVSPVFTGLVISLLENILVIVAIAKNKLNHSPMYFF 82
DB 25 PASNRSGS-----GFCEQVFKPEVFLALGIVSILMENILVILAVVRNGLHSPMYFF 76

QY 83 ICSLAVADMLVSVNSGSETIVITLLNSTD-TDAQSFVNIDNVDSICSSLLASCSLL 141
DB 77 LCSLAADMLVSLNSLETIMTAVINSLSLTDQFIQHMNIDFSDMISIVASICNLL 136

QY 142 STAVDRYFTFYALQYHNIMTVRRVGGIIISCIWAACVSGVLFIIYSDSSAVTICLTWF 201
DB 137 AIAIDRVYTFYALRYSIMTVRKATLIGVIVWCGIGGVFIYSEKMWIVCLITWF 196

QY 202 FTMALMASLYVHMFMARLHKRIAVLPGTGPI--RQGANMKGATTLILIGVFVVCWA 259
DB 197 FAVMLMGLTYIHMFLFARLHVQRIAVLPAGVAPQHQSCMKGAVTITLLIGVTFCWA 256

QY 260 PFELHLFIYSCPNPCYCFMSHFNLYLLIMCNSIIDPLIYALRSQELKTFKEIIC 318
DB 257 PFELHLVLITCTPNTNYCYTAHENTYLVLMCNSVIDPLIYAFRSLELRTFEILC 315

RESULT 10
MC3R_HUMAN
ID MC3R_HUMAN STANDARD; PRT; 360 AA.
AC F41968; Q9H517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Melanocortin-3 receptor (MC3-R).
GN MC3R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93216807; PubMed=8463333;
RA Gantz I., Konda Y., Tashiro T., Shimoto Y., Miwa H., Munzert G.,
RA Watson S.J., Delvalle J., Yamada T.;
RT "Molecular cloning of a novel melanocortin receptor.";
RL J. Biol. Chem. 268:8246-8250(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., A.J.,
RA Beasley O.P., Bird C.P., Blake S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
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RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Showkeen R., Sims S.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Steward C.A., Sulston J.E.,
RA Skuce C.D., Smith M.L., Soderlund C., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Swann R.M., Sycamore N., Vaudin M., Wall M., Wallis J.W., Wray P.W.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.W., Wray P.W.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN, PLACENTAL, AND GUT TISSUES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; L06155; AAC13541.1; -
CC EMBL; AL139824; CAC15480.1; -
CC Genbank; HGNC:6931; MC3R.
CC MIM; 155540; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 74 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 75 100 1 (POTENTIAL).
FT DOMAIN 101 112 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 113 137 2 (POTENTIAL).
FT DOMAIN 138 155 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 156 177 3 (POTENTIAL).
FT DOMAIN 178 197 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 198 218 4 (POTENTIAL).
FT DOMAIN 219 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 247 5 (POTENTIAL).
FT DOMAIN 248 282 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 283 305 6 (POTENTIAL).
FT DOMAIN 306 314 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 315 338 7 (POTENTIAL).
FT DOMAIN 339 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 352 352 PALMITATE (POTENTIAL).
FT CONFLICT 6 6 T -> K (IN REF. 1).
FT CONFLICT 81 81 V -> I (IN REF. 1).
SQ SEQUENCE 360 AA; 40072 MW; 0D2C61195C164C51 CRC64;

Query Match 57.2%; Score 988.5; DB 1; Length 360;
Best Local Similarity 62.0%; Pred. No. 1.8e-58;
Matches 186; Conservative 49; Mismatches 58; Indels 7; Gaps 3;

QY 26 NASESLGKGY-----SDGGCEYOLFVSPVFTGLVISLLENILVIVAIAKNKLNHSPMYFF 81
DB 53 NGEHLQAPFFNSQSSAFCEQVFKPEVFLSILLENILVILAVVRNGLHSPMYFF 112

QY 82 FTCSLAVADMLVSVNSGSETIVITLLNSTD-TDAQSFVNIDNVDSICSSLLASCSL 140
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113 FLCSLAVADMVSVSNALETTIAIVHSYDLTFEDQFOHMDNFDSMICSLVASICNL 172
141 LSIADVRYFTFYALOVHNMVVRVGIISCIWAACVTSVGLFIYISDSSAVICLITM 200
173 LAIAVDRTVITFYALRHSIMTVKATLVAIIVWCGVGVFVIVSESKMWIVCLITM 232
201 FFTMLMASLYVHMFMLRIKRIAPVPGTGI--ROGANMKGAITLTILIGVFFVVCW 258
233 FFAMLLMGTLVHMFLEFARLHVRIAPALPADGVAPOHSCMKGAVTITLLGVFFCW 292
259 APFFLHLFIYISCPONPCVCFMSHFNLYLLIMCNSIIDPLIYALRSQELRKFKEIC 318
293 APFFLHLVLIITCPTNPICYTAHENTYLVLMCNSVIDPLIYAFRSLELRNTRFELC 352

RESULT 11
MC5R_BOVIN
ID MC3R_BOVIN STANDARD; PRT; 325 AA.
AC P56451;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Melanocortin-5 receptor (MC5-R).
GN MC3R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Oulmouden A., Petit J.M., Julien R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 311 311 PALMITATE (POTENTIAL).
SQ SEQUENCE 325 AA; 36525 MW; 81B6ACB2F12A09C7 CRC64;

Query Match 56.3%; Score 972.5; DB 1; Length 325;
Best Local Similarity 58.3%; Pred. NO. 1.9e-57;
Matches 201; Conservative 39; Mismatches 72; Indels 33; Gaps 5;

QY 1 MNSSTHHHGMHTSLHFWRNSTYCPHSNASESLGKGYSDGG-----CYEOLFVSP 48
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 1 MNSSFH-----LHFLD-----LGLNTDGNLSGLSVQNASSLC-EDMGIAV 40
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 49 EVFVTYGLISLENLIVIAIAKKNLHSPWFFICSLAVADMLVSVSGSETIVITLL- 107
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 41 EVFLALGLISLENLIVIGAIVRNENLHTPMYFFVGLAVADMLVSLNSWETIYLLT 100
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 108 NSTDTAQSFVTNIDNIDSVICSLASISLSDIAVDYFTFIYALQYINIMTVRVG 167
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 101 NKHLVMADASVRHLDNVFDSMICISVVASMCSLLAIAVDYVTFPCALRYQRIIMTGRSG 160
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 168 IISCIWAACVTSVGLFIYISDSSNAVIICLITMFTMLALMASLYVHMFMLRIKRIA 227
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 161 AIIIGIWAFCASCCTFVIYVESTYVVICLAMEFLTMLLMASLYTHFLARHRIA 220
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 228 VLPGTGTIGRAGNMKGATITLIGVFFVVCWAPFLHLFIYISCPONPCVCFMSHFNLY 287
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 221 TLPGHSSVRQRTGVKGATITLAMLVGVFVVCWAPFLHLILMISCPHNLVYSCFNSHFNY 280
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
QY 288 LILIMCNSIIDPLIYALRSQELRKFKEICCYPLGGLCDLSRY 332
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |
Db 281 LILIMCNSVIDPLIYAFRSQEMRKTFKEICVFQSFRTPCRFPSPRY 325
   |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: | |||: |

RESULT 12
MC3R_RAT
ID MC3R_RAT STANDARD; PRT; 323 AA.
AC P32244;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Melanocortin-3 receptor (MC3-R).
GN MC3R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Fischer; TISSUE=Hypothalamus;
RX MEDLINE=94022273; PubMed=8415620;
RA Roselli-Rehfuess L., Mountjoy K.G., Robbins L.S., Mortrud M.T.,
RA Low M.J., Simerly R.B., Cone R.D.;
RT "Identification of a receptor for gamma melanotropin and other
RT proopiomelanocortin peptides in the hypothalamus and limbic system.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8856-8860(1993).
CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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Db 293 LIYAFRQEMKTFKEIVCFQGFRTPCRFSTY 325
|||||
RESULT 14
MC5R_PIG STANDARD; PRT; 294 AA.
AC Q9MZV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanocortin-5 receptor (Fragment).
GN MC5R.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus...
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20353873; PubMed=10895318;
RA Kim K.S., Marklund S., Rothschild M.F.;
RT "The proline melanocortin-5 receptor (MC5R) gene: polymorphisms,
RT linkage and physical mapping.";
RL Anim. Genet. 31:230-231(2000).
CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF133793; AAF82610.1; .
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRRHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC NON_TER 1 1
CC DOMAIN <1 29 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 30 53 1 (POTENTIAL).
CC DOMAIN 54 65 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 66 89 2 (POTENTIAL).
CC DOMAIN 90 106 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 107 130 3 (POTENTIAL).
CC DOMAIN 131 147 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 148 171 4 (POTENTIAL).
CC DOMAIN 172 178 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 179 203 5 (POTENTIAL).
CC DOMAIN 204 231 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 232 257 6 (POTENTIAL).
CC DOMAIN 258 265 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 266 289 7 (POTENTIAL).
CC DOMAIN 290 >294 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 12 12 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 20 20 N-LINKED (GLCNAC. .) (POTENTIAL).
CC NON_TER 294 294
CC SEQUENCE 294 AA; 32753 MW; C6ED78FA26B55D42 CRC64;
Query Match 54.38; Score 939; DB 1; Length 294;
Best Local Similarity 63.78; Pred. No. 2.7e-55;
Matches 186; Conservative 40; Mismatches 52; Indels 14; Gaps 4;
QY 26 NASESLGKGYSDGG----CYQLFVSPVEVFTLGLVISLLENILVIVAIAKKNLHSPMYF 81
|||||
Db 7 NATEGNVSQPSVGNTPSPC-EDMGIEVEVFTLGLISLLENILVIGALARNKLNHPVYF 65
82 FICSLAVADMVLVSNGSETIVITLLNS-----TDTAQSTVNDVNDVSDVSSLLAS 136
66 FVCSLAVADMVLVSLSNSWETITIIANKHLVLDTSVSR----HLDNVFDSMISLVS 121
137 ICSSLSTAVDRYFTFYALQYHNIMTVRRVGIIISCIWAACVTSGLFIIYSDSSAVIIC 196
122 MCSLLAVADVRYVTFYALRYOHLMTGRCGAIITAGIWTALCTGCGPFIYVYESTYVVC 181
197 LITMFFTMLALMASLYVHMFLMARLHKRIKRIAVLPETGTIRQGANMKGAITITILIGVYV 256
182 LVAMFLTMLLMSLYAHMFLQARAHVRIIAALPGYRSARQRTSMKGAVTILAMLIGVIV 241
257 CWAPFFHLFIYISCPNQNVCFMPSHFNLYLILIMCNSIIDPLIYALRSOE 308
242 CWAPFFHLFIIMISCPNQNYCSCPMFNFMYLILIMCNSVIDPLIYAFRSOE 293
RESULT 15
MC4R_MOUSE STANDARD; PRT; 184 AA.
AC P56450;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Melanocortin-4 receptor (MC4-R) (Fragment).
GN MC4R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Anterior pituitary;
RA Morooka Y., Oomizu S., Takeuchi S., Takahashi S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO
CC ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA- AND GAMMA-MSH.
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AB009664; BAA24015.1; .
CC MGD; MGI:99457; MC4R.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC phosphorylation; Lipoprotein; Palmitate.
CC NON_TER 1 1
CC DOMAIN <1 12 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 13 34 3 (POTENTIAL).
CC DOMAIN 35 54 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 55 75 4 (POTENTIAL).
CC DOMAIN 76 80 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 81 104 5 (POTENTIAL).
CC DOMAIN 105 137 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 138 160 6 (POTENTIAL).
CC DOMAIN 161 169 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 170 >184 7 (POTENTIAL).
CC NON_TER 184 184
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SQ SEQUENCE 184 AA; 20614 MW; 9C61CAD31BA0DE33 CRC64;  
Query Match 53.9%; Score 932; DB 1; Length 184;  
Best Local Similarity 96.7%; Pred. No. 5.1e-55;  
Matches 178; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 112 TDAQSTVNIDNVIDSVICSSLLASTCSLLSIADVRYFTFYALQYHNIMTVRRVGIIIS 171  
Db 1 TDAQSTVNIDNVIDSVICSSLLASTCSLLSIADVRYFTFYALQYHNIMTVRRVGIIIS 60  
QY 172 CIWAACVSGVLFIYSDSSAVIICLITMFFTMLMASLYVHMFMLMARLHKRIAVLPG 231  
Db 61 CIWAACVSGVLFIYSDSSAVIICLISMFMTMLVLMASLYVHMFMLMARLHKRIAVLPG 120  
QY 232 TGTIRQANMKGAITLTILIGVVCWAPFFLHLIFYISCPONPYCVCFSHFNLVLI 291  
Db 121 TGTIRQGTNNKGAITLTILIGVVCWAPFFLHLIFYISCPONPYCVCFSHFNLVLI 180  
QY 292 MCNS 295  
Db 181 MCNA 184

Search completed: June 4, 2003, 18:16:17  
Job time : 15 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	1657	95.9	332	11	Q9EQM7		Q9eqm7 mus musculus
2	1510.5	87.4	331	13	Q73667		Q73667 gallus gall
3	1161.5	67.2	322	13	Q90X73		Q90x73 takifugu po
4	1161.5	67.2	322	13	Q90YX0		Q90yx0 takifugu ch
5	1156.5	66.9	322	13	Q90X74		Q90x74 takifugu ra
6	1156.5	66.9	322	13	Q90X72		Q90x72 takifugu po
7	1105.5	64.0	325	13	Q73671		Q73671 gallus gall
8	1103	63.8	223	6	Q95L85		Q95lb5 ovis aries
9	1029.5	59.6	325	13	Q93259		Q93259 gallus gall
10	825	47.7	314	13	Q90ZP7		Q90zp7 tangara cuc
11	824	47.7	314	13	Q90VY8		Q90vy8 coereba fla
12	823	47.6	314	13	Q90ZQ0		Q90zq0 coereba fla
13	823	47.6	314	13	Q90VX9		Q90vx9 coereba fla
14	820	47.5	314	13	Q90ZP8		Q90zp8 coereba fla
15	820	47.5	314	13	Q90VY8		Q90vy8 coereba fla
16	818	47.3	314	13	Q90ZP9		Q90zp9 coereba fla

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QY 61 ENILVIAIAKKNLHSPMYFFICSIAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120
Db 61 ENILVIAIAKKNLHSPMYFFICSIAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180
QY 181 GVLFIYSDSSAVIICLTMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GVLFIYSDSSAVIICLTMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
QY 241 MGKAITLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
Db 241 MGKAITLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSRY 332
Db 301 IYALRSQELRKTFKEIICCYPLGGLCDLSRY 332

RESULT 2
073667 PRELIMINARY; PRT; 331 AA.
ID 073667
AC 073667;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE Melanocortin 4-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=LIVER;
RA Takeuchi S., Takahashi S.;
RT "Molecular cloning of the chicken melanocortin 4-receptor gene widely
RT expressed in peripheral tissues.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB012211; BAA25252.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 331 AA; 36984 MW; 98B25F5A1FFB02C1 CRC64;

Query Match 87.4%; Score 1510.5; DB 13; Length 331;
Best Local Similarity 87.3%; Pred. No. 8.1e-125;
Matches 290; Conservative 15; Mismatches 26; Indels 1; Gaps 1;

QY 1 MNSTHHGHMTSLHFWNRSTYCPHNSAESLGKGYDGGCYEQLFVSPFVTLGVISLL 60
Db 1 MNSTHHGHMTSLHFWNRSTYCPHNSAESLGKGYDGGCYEQLFVSPFVTLGVISLL 60
QY 1 MNFTQHRGTLPQLEFWNOSN-GLHRGASEPSAKSHSGGCGYEQLFVSPFVTLGVISLL 59
Db 1 MNFTQHRGTLPQLEFWNOSN-GLHRGASEPSAKSHSGGCGYEQLFVSPFVTLGVISLL 59
QY 61 ENILVIAIAKKNLHSPMYFFICSIAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120
Db 61 ENILVIAIAKKNLHSPMYFFICSIAVADMLVSVNGSETIVITLLNSTDDAQSFVN 119
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 180
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGGIISCIWAACVTS 179
QY 181 GVLFIYSDSSAVIICLTMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240
Db 181 GVLFIYSDSSAVIICLTMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 239
QY 241 MGKAITLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
Db 241 MGKAITLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 300
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Db 240 MGKAITLTILIGVVCWAPFFLHLIFYISCPNYPYCVCFMSHFNYLILIMCNSIIDPL 299
QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSRY 332
Db 301 IYALRSQELRKTFKEIICCYPLGGLCDLPCKY 331

RESULT 3
Q90V73 PRELIMINARY; PRT; 322 AA.
ID Q90V73
AC Q90V73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu porphyreus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176187;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073677; BAB71733.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1.2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35948 MW; A16712C763F91236 CRC64;

Query Match 67.2%; Score 1161.5; DB 13; Length 322;
Best Local Similarity 76.5%; Pred. No. 3.7e-94;
Matches 218; Conservative 31; Mismatches 35; Indels 1; Gaps 1;

QY 36 SDGGCYEQLFVSPFVTLGVISLLLENILVIAIAKKNLHSPMYFFICSIAVADMLVSV 95
Db 31 SSTGCGEQLMISTEVEFTLGISLLENILVIAIAKKNLHSPMYFFICSIAVADMLVSV 90
QY 96 SNGSETIVITLLNS-TDDAQSFVNIDNVDSVICSSLLASICSLLSTAVDRYFTIFY 154
Db 91 SNASETIVIALINSGTLTIPATLIKSMNDVFDSDMICSSLLASICSLLSTAVDRYFTIFY 150
QY 155 LQYHNIMTVRRVGGIISCIWAACVTSGLVFIYSDSSAVIICLTMTLMALMASLYVH 214
Db 151 LRYHNITVTLRRASLVSISSITWCCTVSGVLFIYVSESTVTLICLTITMFTMLVLMASLYVH 210
QY 215 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVVCWAPFFLHLIFYISCPON 274
Db 211 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVVCWAPFFLHLILMITCPKN 270
QY 275 PYCVCFMSHFNYLILIMCNSIIDPLIYALRSQELRKTFKEIICC 319
Db 271 PYCTCFMSHFNYLILIMCNSIIDPLIYAFRSQEMRKTFKEIFCC 315

RESULT 4
Q90VY0 PRELIMINARY; PRT; 322 AA.
ID Q90VY0
AC Q90VY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu chinensis, and
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176185, 31033;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=T.chinensis, and F.rubripes;
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RL gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073675; BAB71731.1; -
DR EMBL; AB073674; BAB71730.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35975 MW; 8AF03A6371F5E1F6 CRC64;

Query Match 67.28; Score 1161.5; DB 13; Length 322;
Best Local Similarity 76.58; Pred. No. 3.7e-94;
Matches 218; Conservative 31; Mismatches 35; Indels 1; Gaps 1;

Qy 36 SDGCGYEQLFVSPFVFTLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMLVSV 95
Db 31 SSTCYEQMLISTEVFTLGLIISLLENILVVAIVKKNLHSPMYFFICSLAVADMLVSV 90

Qy 96 SNGSETIVITLLNS-TDTDAQSFVNIDNVSDVICSSLLASICSLLSIAVDRTYTIYA 154
Db 91 SNASETIVIALINSGLTIPATLIKSDMNVFDSMICSSLLASICSLLAIAVDRTYTIYA 150

Qy 155 LOYHNIMTVRVGIIISCIWAACVSGVLFIYSDSSAVIICLITMFTMLMASLVVH 214
Db 151 LRYHNIVTLRRASLVSIISWTCCVSGVLFIYSESTVLCITMFTMLMASLVVH 210

Qy 215 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLFIYISCPQN 274
Db 211 MFLARLHKRIAMPGNAPHQANLKGATLTILIGVFVVCWAPFFLHLILMITCPKN 270

Qy 275 PYCVCFSHNFYLIILIMCNSIIDPLIYALRSQELRTFKEIICC 319
Db 271 PYCTCFMSHNFYLIILIMCNSVIDPIIYAFRSQEMRKTKEIFCC 315

RESULT 5
Q90Y74 PRELIMINARY; PRT; 322 AA.
ID Q90Y74;
AC Q90Y74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu radiatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176186;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RL gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073676; BAB71732.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35917 MW; 37A8339FDCD84C38 CRC64;
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Query Match 66.98; Score 1156.5; DB 13; Length 322;
Best Local Similarity 76.18; Pred. No. 1e-93;
Matches 217; Conservative 31; Mismatches 36; Indels 1; Gaps 1;

Qy 36 SDGCGYEQLFVSPFVFTLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMLVSV 95
Db 31 SSTCYEQMLISTEVFTLGLIISLLENILVVAIVKKNLHSPMYFFICSLAVADMLVSV 90

Qy 96 SNGSETIVITLLNS-TDTDAQSFVNIDNVSDVICSSLLASICSLLSIAVDRTYTIYA 154
Db 91 SNASETIVIALINSGLTIPATLIKSDMNVFDSMICSSLLASICSLLAIAVDRTYTIYA 150

Qy 155 LOYHNIMTVRVGIIISCIWAACVSGVLFIYSDSSAVIICLITMFTMLMASLVVH 214
Db 151 LRYHNIVTLRRASLVSIISWTCCVSGVLFIYSESTVLCITMFTMLMASLVVH 210

Qy 215 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLFIYISCPQN 274
Db 211 MFLARLHKRIAMPGNAPHQANLKGATLTILIGVFVVCWAPFFLHLILMITCPKN 270

Qy 275 PYCVCFSHNFYLIILIMCNSIIDPLIYALRSQELRTFKEIICC 319
Db 271 PYCTCFMSHNFYLIILIMCNSVIDPIIYAFRSQEMRKTKEIFCC 315

RESULT 6
Q90Y72 PRELIMINARY; PRT; 322 AA.
ID Q90Y72;
AC Q90Y72;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu poecilnotus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176188;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RL gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073678; BAB71734.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35945 MW; 1C3F1B3BCED4BFF8 CRC64;

Query Match 66.98; Score 1156.5; DB 13; Length 322;
Best Local Similarity 76.18; Pred. No. 1e-93;
Matches 217; Conservative 31; Mismatches 36; Indels 1; Gaps 1;

Qy 36 SDGCGYEQLFVSPFVFTLGVISLLENILVIAIAKKNLHSPMYFFICSLAVADMLVSV 95
Db 31 SSTCYEQMLISTEVFTLGLIISLLENILVVAIVKKNLHSPMYFFICSLAVADMLVSV 90

Qy 96 SNGSETIVITLLNS-TDTDAQSFVNIDNVSDVICSSLLASICSLLSIAVDRTYTIYA 154
Db 91 SNASETIVIALINSGLTIPATLIKSDMNVFDSMICSSLLASICSLLAIAVDRTYTIYA 150

Qy 155 LOYHNIMTVRVGIIISCIWAACVSGVLFIYSDSSAVIICLITMFTMLMASLVVH 214
Db 151 LRYHNIVTLRRASLVSIISWTCCVSGVLFIYSESTVLCITMFTMLMASLVVH 210

Qy 215 MFLMARLHKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLFIYISCPQN 274
Db 211 MFLARLHKRIAMPGNAPHQANLKGATLTILIGVFVVCWAPFFLHLILMITCPKN 270
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Db 14 SNAEGHNSNATVAGGWCQ-----LDIPNELFLALGLVSLVENLLVVAAILKRNHLH 68  
QY 77 SPMYFFICSLAVADMLVSVNGSEITVITLL-NSTDIDAQSFNTVDNVIDSVICSSLLA 135  
Db 69 SPTYFFICCLAVSDMLVSLNLAEMFLMLLEHGLVLMRPSIVRHMSVDITLICSSVVS 128  
QY 136 SICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVSGVLFIYSDSSAVII 195  
Db 129 SLSFLGVIAVDRIYITFYALRYHSIMTLQRAVVTWASVWLASTVSTVLIYRNTILL 188  
QY 196 CLITMEFTMALMASLYVHMETLMARLHKRIKRIAVLPCTGTIROGANKMGAITLILGVFV 255  
Db 189 CLIGFLFMLVLMVLYIHMFLARHLSHSISQQPPTAHRGSLUGKAVTILILGVFF 248  
QY 256 VCMAPFHLFIYISCPQNPYCVCFMSHFNLIILIMCNSIIDPLIYALRSQELRKTKE 315  
Db 249 ICWGPFFHLLIVTCPTNPFCACFYSFNFLLIILICNSVIDPLIYAFRSQELRRTLE 308  
QY 316 IICC 319  
Db 309 VVTC 312

## RESULT 12

Q90200 PRELIMINARY; PRT; 314 AA.  
ID Q90200  
AC Q90200  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Melanocortin 1 receptor.  
OS Coereba flaveola (banaquit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;  
OC Fringillidae; Emberizinae; Coereba.  
OX NCBI\_TaxID=87177;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21261843; PubMed=11369199;  
RA Theron E., Hawkins K., Birmingham E., Ricklefs R.E., Mundy N.I.;  
RT "The molecular basis of an avian plumage polymorphism in the wild: a  
RT melanocortin-1-receptor point mutation is perfectly associated with  
RT the melanic plumage morph of the bananaquit, Coereba flaveola."  
RL Curr. Biol. 11:550-557(2001).  
DR EMBL; AF362584; AAK50791.1; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 314 AA; 34998 MW; 2174CD2BE615BAEB CRC64;

Query Match 47.6%; Score 823; DB 13; Length 314;  
Best Local Similarity 50.3%; Pred. No. 2e-64;  
Matches 153; Conservative 65; Mismatches 80; Indels 6; Gaps 2;

QY 17 NRSTYGPISHNASESLGKYGCGEQFLVSPDEVFTLGVISLLENILVIVAIAKKNLH 76  
Db 14 SNAEGHNSNATVAGGWCQ-----LDIPNELFLALGLVSLVENLLVVAAILKRNHLH 68  
QY 77 SPMYFFICSLAVADMLVSVNGSEITVITLL-NSTDIDAQSFNTVDNVIDSVICSSLLA 135  
Db 69 SPTYFFICCLAVSDMLVSLNLAEMFLMLLEHGLVLMRPSIVRHMSVDITLICSSVVS 128  
QY 136 SICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVSGVLFIYSDSSAVII 195  
Db 129 SLSFLGVIAVDRIYITFYALRYHSIMTLQRAVVTWASVWLASTVSTVLIYRNTILL 188  
QY 196 CLITMEFTMALMASLYVHMETLMARLHKRIKRIAVLPCTGTIROGANKMGAITLILGVFV 255  
Db 189 CLIGFLFMLVLMVLYIHMFLARHLSHSISQQPPTAHRGSLUGKAVTILILGVFF 248  
QY 256 VCMAPFHLFIYISCPQNPYCVCFMSHFNLIILIMCNSIIDPLIYALRSQELRKTKE 315

Db 249 ICWGPFFHLLIVTCPTNPFCACFYSFNFLLIILICNSVIDPLIYAFRSQELRRTLE 308  
QY 316 IICC 319  
Db 309 VVTC 312  
RESULT 13  
Q90VX9 PRELIMINARY; PRT; 314 AA.  
ID Q90VX9  
AC Q90VX9  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Melanocortin 1 receptor.  
OS Coereba flaveola (banaquit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;  
OC Fringillidae; Emberizinae; Coereba.  
OX NCBI\_TaxID=87177;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21261843; PubMed=11369199;  
RA Theron E., Hawkins K., Birmingham E., Ricklefs R.E., Mundy N.I.;  
RT "The molecular basis of an avian plumage polymorphism in the wild: a  
RT melanocortin-1-receptor point mutation is perfectly associated with  
RT the melanic plumage morph of the bananaquit, Coereba flaveola."  
RL Curr. Biol. 11:550-557(2001).  
DR EMBL; AF362583; AAK50790.1; -  
DR EMBL; AF362578; AAK50785.1; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 314 AA; 35024 MW; 8BDA7D205AA4675A CRC64;

Query Match 47.6%; Score 823; DB 13; Length 314;  
Best Local Similarity 50.3%; Pred. No. 2e-64;  
Matches 153; Conservative 65; Mismatches 80; Indels 6; Gaps 2;

QY 17 NRSTYGPISHNASESLGKYGCGEQFLVSPDEVFTLGVISLLENILVIVAIAKKNLH 76  
Db 14 SNAEGHNSNATVAGGWCQ-----LDIPNELFLALGLVSLVENLLVVAAILKRNHLH 68  
QY 77 SPMYFFICSLAVADMLVSVNGSEITVITLL-NSTDIDAQSFNTVDNVIDSVICSSLLA 135  
Db 69 SPTYFFICCLAVSDMLVSLNLAEMFLMLLEHGLVLMRPSIVRHMSVDITLICSSVVS 128  
QY 136 SICSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVSGVLFIYSDSSAVII 195  
Db 129 SLSFLGVIAVDRIYITFYALRYHSIMTLQRAVVTWASVWLASTVSTVLIYRNTILL 188  
QY 196 CLITMEFTMALMASLYVHMETLMARLHKRIKRIAVLPCTGTIROGANKMGAITLILGVFV 255  
Db 189 CLIGFLFMLVLMVLYIHMFLARHLSHSISQQPPTAHRGSLUGKAVTILILGVFF 248  
QY 256 VCMAPFHLFIYISCPQNPYCVCFMSHFNLIILIMCNSIIDPLIYALRSQELRKTKE 315  
Db 249 ICWGPFFHLLIVTCPTNPFCACFYSFNFLLIILICNSVIDPLIYAFRSQELRRTLE 308  
QY 316 IICC 319  
Db 309 VVTC 312

## RESULT 14

Q902P8 PRELIMINARY; PRT; 314 AA.  
ID Q902P8  
AC Q902P8  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

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DR EMBL; AF362603; AAK50810.1; -.
DR EMBL; AF362601; AAK50808.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 314 AA; 35037 MW; 666E3AA712D7409C CRC64;
      Query Match 47.5%; Score 820; DB 13; Length 314;
      Best Local Similarity 50.3%; Pred. No. 3.7e-64;
      Matches 153; Conservative 65; Mismatches 80; Indels 6; Gaps 2;
QY 17 NRSTYGPHSNASESLGKGYSDGGCYQQLFVSPPEVFTLVGLVISLLENILVIVATAKNKHLH 76
Db : : | | | | : | | : | | : | : | : | : | : | : | : | : | : | : | : |
14 SNASEGNHNSNATVGAGGGWCQG-----LDIPNELFLALGLVSLVENLLVVAAILKNRNLH 68
QY 77 SPMYFFTCISLAVADMVLSVSYNGSETIVITLL-NSTDYDAQSFVNTINDVIDSVICSSLLA 135
Db || | | | | | | | | | | | | : : : | | : | : | : | : | : | : | : | :
69 SPYYFICCLAVSDMLVSISSNLAKMFLMLLLEHGVLMRPSIVRHMDSVIDTLICSSVWS 128
QY 136 SICSLLSIAVDYFTIFYALQYINIMTVRRVGIISCIWAACTVSGVLFTIYSDSAVII 195
Db | : | | | | | | | | | | | | : : : | | | : | | : | : | : | : | : |
129 SLSEFLGVIAVDYITIFYALRYHSIMTLQRAVTVMASVWLASTVSTLVITYYRSNTILL 188
QY 196 CLITMFTFMALMASLYVMFMFLMARLHRIKRIAVLPGTGTIRQANKMGATLLILIGVFV 255
Db || | | | | | | | | | | | | : : | : | : | : | : | : | : | : | : |
189 CLIGFFLEFLVLMVLVLYIHMFALARHLLHSISSQQKPPPTAHRGGSLKGAVTLTLLGVFF 248
QY 256 VCAWPFELHLIFVISCQPNPCYCVCFMSHENXLYLLIMCNSIIDPLIYALRSQELRKFKE 315
Db || | | | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
249 ICMGPFHLLILIVTCTNPNFCFFSYFNLFLILICNSVIDPLIYAFRSQELRRTLRE 308
QY 316 IICC 319
Db : : |
309 VVTC 312
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Job time : 54 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 4, 2003, 17:58:11 ; Search time 12.5 seconds  
(without alignments)  
781.473 Million cell updates/sec

Title: US-09-884-211A-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKRIICYPGLGGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1638.5	94.9	332	1	US-08-671-525B-8
2	1638.5	94.9	332	1	US-08-672-109B-8
3	1638.5	94.9	332	2	US-08-842-045-8
4	1638.5	94.9	332	2	US-08-842-045-8
5	1638.5	94.9	332	2	US-08-842-238-8
6	1638.5	94.9	332	3	US-08-780-749A-2
7	1638.5	94.9	332	3	US-08-629-335B-8
8	1638.5	94.9	332	4	US-08-870-511-2
9	1632.5	94.6	332	2	US-09-384-302A-9
10	1632.5	94.6	332	2	US-08-662-560-2
11	1632.5	94.6	332	2	US-08-780-749A-6
12	1632.5	94.6	332	4	US-08-870-511-6
13	1627.5	94.3	332	4	US-08-870-511-8
14	1626.5	94.2	332	4	US-08-870-511-10
15	1615.5	93.6	332	4	US-08-870-511-12
16	1592.5	92.3	332	3	US-09-384-302A-6
17	1592.5	92.3	332	3	US-08-706-281A-16
18	1405	81.4	293	4	US-09-057-231-16
19	1026.5	59.5	325	3	US-09-384-302A-8
20	1026.5	59.5	325	3	US-08-706-281A-18
21	1023.5	59.3	325	1	US-09-097-231-18
22	1023.5	59.3	325	1	US-08-671-525B-10
23	1023.5	59.3	325	1	US-08-672-109B-10
24	1023.5	59.3	325	2	US-08-842-045-10
25	1023.5	59.3	325	3	US-08-842-238-10
26	1003.5	58.1	325	4	US-08-629-335B-10
27	981.5	56.9	360	1	US-08-387-805-16

28	981.5	56.9	360	1	US-08-672-109B-6	Sequence 6, Appli
29	981.5	56.9	360	2	US-08-842-045-6	Sequence 6, Appli
30	981.5	56.9	360	2	US-08-842-238-6	Sequence 6, Appli
31	981.5	56.9	360	2	US-08-780-749A-1	Sequence 1, Appli
32	981.5	56.9	360	3	US-08-629-335B-6	Sequence 6, Appli
33	981.5	56.9	360	4	US-08-870-511-1	Sequence 1, Appli
34	965	55.9	323	2	US-08-044-812A-4	Sequence 4, Appli
35	965	55.9	323	2	US-08-475-637-4	Sequence 4, Appli
36	965	55.9	323	4	US-09-191-359-4	Sequence 4, Appli
37	961	55.7	323	3	US-08-706-281A-12	Sequence 12, Appli
38	961	55.7	323	4	US-09-097-231-12	Sequence 12, Appli
39	752.5	43.6	315	1	US-07-866-979-4	Sequence 4, Appli
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41	752.5	43.6	315	3	US-08-706-281A-4	Sequence 4, Appli
42	752.5	43.6	315	4	US-09-201-746-4	Sequence 4, Appli
43	752.5	43.6	315	4	US-09-097-231-4	Sequence 4, Appli
44	752.5	43.6	317	4	US-08-387-805-2	Sequence 2, Appli
45	751.5	43.5	317	1	US-07-866-979-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-08-671-525B-8  
; Sequence 8, Application US/08671525B  
; Patent No. 5703220  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/671,525B  
; APPLICATION NUMBER: US/08/671,525B  
; FILING DATE: June 27, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-671-525B-8

Query Match	94.9%	Score	1638.5	DB	1	Length	332		
Best Local Similarity	95.5%	Pred.	No. 4.8e-126						
Matches	317	Conservative	6	Mismatches	8	Indels	1	Gaps	1
QY	1	MNSTLQHGHTSLHFWNRSTYGQGNATSLGKGYPDGCVYQQLFVSPFVTLGVISLL	60						
Db	2	VNST-HRGMTSLHFWNRSTRLHNSASESLGKGYSDGGCVYQQLFVSPFVTLGVISLL	60						
QY	61	ENTLVIVIAIKNNKLNHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDTDAQSFTVN	120						

Db	61	ENILVIVATAKKNKHLSPWFFICSLAVADMLVSVNGSETIIITLNSTDDTDAQSFYN	120
Qy	121	IDNVDSVICSSLLASICSLLSIAVDRTFTIFYALQYHNMTVRRVGGIIISCIIWAAC	180
Db	121	IDNVDSVICSSLLASICSLLSIAVDRTFTIFYALQYHNMTVKRVGGIIISCIIWAAC	180
Qy	181	GILFIYSDSTAVIICLTIMFETMALMASLYVHFMFLMARLHKRTAVLPGTCTIRQ	240
Db	181	GILFIYSDSSAVIICLTIMFETMALMASLYVHFMFLMARLHKRTAVLPGTGAIRQ	240
Qy	241	MKGATLTILIGVFVVCWAPFELHLIFVISPQNPYCVCFMSHFNLYLILIMCNSIID	300
Db	241	MKGATLTILIGVFVVCWAPFELHLIFVISPQNPYCVCFMSHFNLYLILIMCNSIID	300
Qy	301	IYALRSQELRKTFKEIICCYPLGGLCDLSRRY	332
Db	301	IYALRSQELRKTFKEIICCYPLGGLCDLSRRY	332

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RESULT 2
US-08-672-109B-8
; Sequence 8, Application US/08672109B
; Patent No. 5710265
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors

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Query Match      94.9%; Score 1638.5; DB 1; Length 332;
Best Local Similarity 95.5%; Pred. No. 4.8e-126;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGMHTSLHFWRNSTYQGHNATESLGRGYDGGCYEQLFVSPVEFVTLGVISLL 60
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Db 2 VNST-HRCGMHTSLHLWNRSSVRLHNSASESLGRGYSDGGCYEQLFVSPVEFVTLGVISLL 60

QY 61 ENILVIVAIAKKNLHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDQASFTVN 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFTCISLAVADMLVSVNSGSETIIITLLNSTDQASFTVN 120
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QY 121 IDNWIDSVICSSLLASTCSLLSTANVDRYFTFYALQYHNMIVRRVGGIIISCIWAACTVS 180
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Db	181	GILFIYSDSSAVICILITMFTMLALMASLVVHMFMARLHKRIAVLPGTGATIQGAN	240
Qy	241	MKGAITLTILIGVFVWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL	300
Db	241	MKGAITLTILIGVFVWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL	300
Qy	301	IYALRSQELRKTFFKEIICCCYPLGGCLDSRRY	332
Db	301	IYALRSQELRKTFFKEIICCCYPLGGCLDSRRY	332

RESULT 3  
US-08-842-045-8  
; Sequence 8, Application US/08842045  
; Patent No. 5817787

	Query Match	94.9%	Score 1638.5	DB 2	Length 332	
	Best Local Similarity	95.5%	Pred. No. 4.8e-136			
	Matches 317	Conservative 6	Mismatches 18	Indels 1	Gaps 1	
Qy	1	MNSTLQGHMITSLHFWMNRSTYGGQHGHNATESLGKGYDPDGGCYEQFLFVSPEVFTLGVISLL	60			
Db	2	VNST-HRGMTSLHLWNRSSYRLHNSNASESLGKGYSDGGCYEQFLFVSPEVFTLGVISLL	60			
Qy	61	ENILIVIAIAKNNLHSPWFFTCISLAVADMVSVNGSETIVITLLNSTDTDAQSFVN	120			
Db	61	ENILIVIAIAKNNLHSPWFFTCISLAVADMVSVNGSETIIITLLNSTDTDAQSFVN	120			
Qy	121	IDNVDSVIGCSLLASTCSLLSIAVDRYFTIFYALQYHNIMTVRRVGIIISCIWAACVPS	180			
Db	121	IDNVDSVIGCSLLASTCSLLSIAVDRYFTIFYALQYHNIMTVRRVGIIISCIWAACVPS	180			
Qy	181	GILFIYSDSTAVIICITIMFFFTMLMASLYVHMFMLRHKKRIAVLPCTGTROGAN	240			



Db 181 MGKAITLILIGVFWVWAPFFLHLIFVISCPOPNVCVCFMSHFNLYLILIMCNSIIDPL 240  
Qy 241 MGKAITLILIGVFWVWAPFFLHLIFVISCPOPNVCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MGKAITLILIGVFWVWAPFFLHLIFVISCPOPNVCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332

RESULT 4  
US-08-842-238-8  
; Sequence 8, Application US/08842238  
; Patent No. 5869257  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/842,238  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-842-238-8

Query Match 94.9%; Score 1638.5; DB 2; Length 332;  
Best Local Similarity 95.5%; Pred. No. 4.8e-126;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
Qy 1 MNSTLQHGMTSLHFVNRSTYGOHGNATESLGRKGYDPGGCYEQLFVSPVEVTLGVLSLL 60  
Db 2 VNST-HRGMHTSLHLNRRSRLHNSASESLGRKGYSDGGCYEQLFVSPVEVTLGVLSLL 60  
Qy 61 ENILVIVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120  
Db 61 ENILVIVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120  
Qy 121 IDNVDSVICSSLLASCISLLSTAVDRYFTIFVALQYHNMTVRRVGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASCISLLSTAVDRYFTIFVALQYHNMTVRRVGIISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVTICLITMFFTMALMASLYVHMFMLARLHKRIAVLPCTGTGAIROGAN 240  
Db 181 GILFIYSDSTAVTICLITMFFTMALMASLYVHMFMLARLHKRIAVLPCTGTGAIROGAN 240  
Qy 241 MGKAITLILIGVFWVWAPFFLHLIFVISCPOPNVCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MGKAITLILIGVFWVWAPFFLHLIFVISCPOPNVCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGLCDLSRY 332

RESULT 5  
US-08-780-749A-2  
; Sequence 2, Application US/08780749A  
; Patent No. 5932779  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank  
; APPLICANT: Huszar, Dennis  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/780,749A  
; FILING DATE: 08-JAN-1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Laura A. Coruzzi  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-780-749A-2

Query Match 94.9%; Score 1638.5; DB 2; Length 332;  
Best Local Similarity 95.5%; Pred. No. 4.8e-126;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
Qy 1 MNSTLQHGMTSLHFVNRSTYGOHGNATESLGRKGYDPGGCYEQLFVSPVEVTLGVLSLL 60  
Db 2 VNST-HRGMHTSLHLNRRSRLHNSASESLGRKGYSDGGCYEQLFVSPVEVTLGVLSLL 60  
Qy 61 ENILVIVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120  
Db 61 ENILVIVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120  
Qy 121 IDNVDSVICSSLLASCISLLSTAVDRYFTIFVALQYHNMTVRRVGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASCISLLSTAVDRYFTIFVALQYHNMTVRRVGIISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVTICLITMFFTMALMASLYVHMFMLARLHKRIAVLPCTGTGAIROGAN 240  
Db 181 GILFIYSDSTAVTICLITMFFTMALMASLYVHMFMLARLHKRIAVLPCTGTGAIROGAN 240  
Qy 241 MGKAITLILIGVFWVWAPFFLHLIFVISCPOPNVCVCFMSHFNLYLILIMCNSIIDPL 300

Db 241 MKGATITLILGVVVCWAPFFHLIFYISCPQNPYCVCFMSHFNLYLILMCNSIIDPL 300

QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
|||||

Db 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

RESULT 6  
US-08-629-335B-8  
; Sequence 8, Application US/08629335B  
; Patent No. 6117975  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/629,335B  
; FILING DATE: July 23, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-629-335B-8

Query Match 94.9%; Score 1638.5; DB 3; Length 332;  
Best Local Similarity 95.5%; Pred. No. 4.8e-126;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLKGYPDGGCYEQLFVSPFVTLGVISLL 60  
:|||||

Db 2 VNST-HRGHMTSLHLNRSYRLHNSASESLGKYSDDGCEQLFVSPFVTLGVISLL 60  
:|||||

QY 61 ENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
:|||||

Db 61 ENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
:|||||

QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFALQYHNIMTVRRVGGIISCIWAACVTS 180  
:|||||

Db 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFALQYHNIMTVRRVGGIISCIWAACVTS 180  
:|||||

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||

Db 181 GILFIYSDSSAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||

QY 241 MKGATITLILGVVVCWAPFFHLIFYISCPQNPYCVCFMSHFNLYLILMCNSIIDPL 300  
:|||||

Db 241 MKGATITLILGVVVCWAPFFHLIFYISCPQNPYCVCFMSHFNLYLILMCNSIIDPL 300  
:|||||

QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332  
|||||

Db 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

RESULT 8  
US-09-384-302A-9  
; Sequence 9, Application US/09384302A  
; Patent No. 6451543  
; GENERAL INFORMATION:  
; APPLICANT: Kochendoerfer, Gerd G  
; APPLICANT: Hunter, Christie L  
; APPLICANT: Kent, Stephen B.H.  
; APPLICANT: Botti, Paolo  
; APPLICANT: Gryphon Sciences  
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis  
; FILE REFERENCE: grfn-028/02WO  
; CURRENT APPLICATION NUMBER: US/09/384,302A  
; PRIOR FILING DATE: 1999-08-26  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 30



```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-780-749A-6

Query Match          94.6%; Score 1632.5; DB 2; Length 332;
Best Local Similarity 95.2%; Pred. No. 1.5e-125;
Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLFVSPFVTLGVISLL 60
DB 2 VNST-HRGHMTSLHLNRRSSYRLHSNASESLGKGYSDGGCYEQLFVSPFVTLGVISLL 60
QY 61 ENILVIVAIAKKNKLNHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
DB 61 ENILVIVAIAKKNKLNHSPMYFFICSLAVADMLVSVSNGSETIIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180
DB 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTIMFTTLMALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
DB 181 GILFIYSDSTAVIICLTIMFTTLMALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
QY 241 MKGATITLTILIGVFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
DB 241 MKGATITLTILIGVFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
DB 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 11
US-08-870-511-6
; Sequence 6, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-870-511-6

Query Match          94.3%; Score 1627.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 3.8e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLFVSPFVTLGVISLL 60
DB 2 VNST-HRGHMTSLHLNRRSSYRLHSNASESLGKGYSDGGCYEQLFVSPFVTLGVISLL 60
QY 61 ENILVIVAIAKKNKLNHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
DB 61 ENILVIVAIAKKNKLNHSPMYFFICSLAVADMLVSVSNGSETIIITLLNSTDTDAQSFTVN 120
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180
DB 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTIMFTTLMALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
DB 181 GILFIYSDSTAVIICLTIMFTTLMALMASLVVHMFMLARLHKRIAVLPGTGTIROGAN 240
QY 241 MKGATITLTILIGVFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
DB 241 MKGATITLTILIGVFVVCWAPFELHLIFYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332
DB 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332

RESULT 13
US-08-870-511-10
; Sequence 10, Application US/08870511
; Patent No. 6287763
```

```
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-10

Query Match          94.2%; Score 1626.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 4.6e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYDGGCYEQLFVSPVFTLGVISLL 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYDGGCYEQLFVSPVFTLGVISLL 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 IYALRSQELRKTFRKIIICYPPLGGCLDLSRY 332
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-384-302A-6
; Sequence 6, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; TITLE OF INVENTION: of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-384-302A-6

Query Match          93.6%; Score 1615.5; DB 4; Length 332;
Best Local Similarity 94.6%; Pred. No. 3.6e-124;
Matches 314; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYDGGCYEQLFVSPVFTLGVISLL 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYIEGRCYEQLFVSPVFTLGVISLL 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query Match          94.2%; Score 1626.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 4.6e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYDGGCYEQLFVSPVFTLGVISLL 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYDGGCYEQLFVSPVFTLGVISLL 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 IDNVDSVICSSLLASICSLLSIAVDRTFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLMARLHRIKRIAVLPGTGTROGAN 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 MKGATLTILIGVFWVWAPFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300
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RESULT 14
US-08-870-511-12
; Sequence 12, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-12

Query Match          94.2%; Score 1626.5; DB 4; Length 332;
Best Local Similarity 94.9%; Pred. No. 4.6e-125;
Matches 315; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MNSTLQHCWHTSLHFWNRSTYCGHGNATESLGKGYDGGCYEQLFVSPVFTLGVISLL 60
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Search completed: June 4, 2003, 18:03:57  
Job time : 14 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:47:14 ; Search time 3506 Seconds  
(without alignments)  
16477.202 Million cell updates/sec

Title: US-09-884-211a-2  
Perfect score: 1985  
Sequence: 1 ctaagaccgtggggaggcag.....gaataaaaaaaaaaaaaa 1985

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
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- 11: gb\_sts.\*
- 12: gb\_sy.\*
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- 15: em\_ba.\*
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- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
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- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1165.6	58.7	1708	6	AX342681	AX342681 Sequence	
3	1060.2	53.4	2113	4	AB021664	AB021664 Sus scrofa	
C	4	1012.4	51.0	161822	2	AP001645	AP001645 Homo sapi
	5	1012.4	51.0	162600	9	AC091576	AC091576 Homo sapi
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17	817.4	41.2	996	6	I87362	I87362 Sequence 7	
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44	429.2	21.6	183619	2	AC111069	AC111069 Mus muscu	
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ALIGNMENTS

RESULT 1  
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LOCUS AX342682 1985 bp DNA linear PAT 12-JAN-2002  
DEFINITION Sequence 2 from Patent EP1167386.  
ACCESSION AX342682  
VERSION AX342682.1 GI:18152062  
KEYWORDS dog.  
SOURCE Canis familiaris  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1  
REFERENCE Hickman, M.A., Houseknecht, K.L. and Robertson, A.S.  
AUTHORS Canine and feline melanocortin-4 receptor sequences and screening  
TITLE assays to identify compounds useful in regulating animal appetite

JOURNAL		and metabolic rate	
Patent: EP 1167386-A 2 02-JAN-2002;		Patent: EP 1167386-A 2 02-JAN-2002;	
Pfizer Products Inc. (US)		Pfizer Products Inc. (US)	
FEATURES		Location/Qualifiers	
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ACCESSION  
AB021664  
VERSION  
AB021664.1 GI:4062864  
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MC4R:  
SOURCE  
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ORGANISM  
Sus scrofa  
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
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Ito.Y. and Minezawa.M.  
Sus scrofa melanocortin 4 receptor gene, complete cds [genomic]  
Published Only in DataBase (1998)  
2 (bases 1 to 2113)  
Ito.Y. and Minezawa.M.  
Direct Submission  
Submitted (21-DEC-1998) Yoshiyasu Ito, National Institute of Animal  
Industry, Animal Genome Research Team; 2 Ikenodai, Kuzizaki-machi,  
Inashiki-gun, Ibaragi 305-0901, Japan  
(E-mail:yoshiito@nia.affrc.go.jp, Tel:81-298-38-8627)  
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BASE COUNT 609 a 463 c 432 g 609 t  
ORIGIN

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Best Local Similarity 78.2%; Pred. No. 7.4e-227;  
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DEFINITION DRAFT SEQUENCE, 7 unordered pieces.
ACCESSION AP001645
VERSION    AP001645.3 GI:9188511
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAPT.
SOURCE     Homo sapiens DNA, clone:RP11-711110.
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 161822)
            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Homo sapiens 161,822 genomic DNA of 18q21
            Published Only in Database (2000)
REFERENCE  2 (bases 1 to 161822)
            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Direct Submission
            Submitted (05-APR-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-15-1 Kikassato, Sagamihara, Kanagawa 228-8555, Japan
            (E-mail:hattori@psc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-42-778-9923, Fax:81-42-778-9924)
            On Jul 14, 2000 this sequence version replaced gi:8117427.
COMMENT     ----- Genome Center
            Center: RIKEN Genomic Sciences Center(GSC)
            Center code: RIKEN
            Web site: http://hgp.gsc.riken.go.jp/
            Contact: hattori@psc.riken.go.jp
            ----- Project Information
            Center project name: HumDraft18
            Center clone name: RP11-711110
            ----- Summary Statistics
            Sequencing vector: PCR products; 100% of reads
            Chemistry: Dye-terminator ET-amersham; 100% of reads

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Assembly program: Phrap; version 0.990329
Consensus quality: 159458 bases at least Q40
Consensus quality: 160527 bases at least Q30
Consensus quality: 160955 bases at least Q20
Insert size: 16122; sum-of-contigs
Quality coverage: 9.98x in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently consists of
7 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

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95519 121226 contig of 25708 bp in length
121327 139017 contig of 17691 bp in length
139118 150492 contig of 11375 bp in length
150593 158977 contig of 8385 bp in length
159078 161822 contig of 2745 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 56165: contig of 56165 bp in length
* 56166 56265: gap of 100 bp
* 56266 95418: contig of 39153 bp in length
* 95419 95518: gap of 100 bp
* 95519 121226: contig of 25708 bp in length
* 121227 121326: gap of 100 bp
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ORIGIN

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Query Match          51.0%; Score 1012.4; DB 2; Length 161822;
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Matches 1520; Conservative 0; Mismatches 391; Indels 83; Gaps 19;

Qy  12 GGGAGGCGAGCTGATCGGAACATGTGCACGACGATTTCAGTCTGTGGTCGGCGGCAAC 71
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Db  7005 GAGAGGCGAGCGATGTGAGCATGTGCGCACAGATTCTCCATATGGCATGCGACGCTTC 6946

```



AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome 18, clone RP11-711110  
2 (bases 1 to 162600)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,  
Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,  
Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,  
Collins,S., Collymore,A., Cooke,P., DeArelano,K., Dewar,K.,  
Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,  
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,  
Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,  
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,  
Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,  
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,  
Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,  
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,  
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,  
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,  
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,  
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,  
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,  
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 162600)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,  
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,  
Cooke,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,  
Landers,T., Lehoczy,J., Levine,R., Marquis,N., Matthews,C.,  
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,  
Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,  
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,  
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 162600)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,  
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
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Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (24-APR-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
5 (bases 1 to 162600)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
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Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,  
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL  
COMMENT

Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 14, 2002 this sequence version replaced gi:20128089.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L12567  
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Query Match 51.0%; Score 1012.4; DB 9; Length 162600;  
Best Local Similarity 76.2%; Pred. No. 6.8e-216;  
Matches 1520; Conservative 0; Mismatches 391; Indels 83; Gaps 19;

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SOURCE Mus musculus  
ORGANISM house mouse.  
REFERENCE 1 (bases 1 to 196426)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE The sequence of Mus musculus clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 196426)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (14-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE 3 (bases 1 to 196426)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (17-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
COMMENT  
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Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
Contact: submissions@wustl.wustl.edu  
----- Project Information -----  
Center project name: M\_BB0566K14  
----- Summary Statistics -----  
Sequencing vector: M13; 0%  
Chemistry: Dye-primer ET; 100%  
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Assembly program: Phrap; version 0.990319  
Consensus quality: 192945 bases at least Q40  
Consensus quality: 194032 bases at least Q30  
Consensus quality: 194786 bases at least Q20  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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\* 1102 1201: gap of unknown length  
\* 1202 21995: contig of 20794 bp in length  
\* 21996 22095: gap of unknown length  
\* 22096 71743: contig of 49648 bp in length  
\* 71744 71843: gap of unknown length  
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BASE COUNT 378 a 404 c 384 g 474 t

ORIGIN

Query Match 42.4%; Score 840.8; DB 10; Length 1640;

Best Local Similarity 80.1%; Pred. No. 1.1e-177;

Matches 1051; Conservative 0; Mismatches 252; Indels 9; Gaps 5;

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#### RESULT 13

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##### LOCUS

##### DEFINITION

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### MEDLINE

##### PUBMED

##### FEATURES

##### source

##### CDS

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##### BASE COUNT 229 a 243 c 213 g 314 t

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Best Local Similarity 89.2%; Pred. No. 8.4e-173; Matches 883; Conservative 0; Mismatches 107; Indels 0; Gaps 0;									
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Job time : 4230 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:01 ; Search time 31 Seconds  
(without alignments)  
1105.670 Million cell updates/sec

Title: US-09-884-211A-4  
Perfect score: 1726  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1003.5	58.1	325	12	US-10-052-545-16
5	994	57.6	323	10	US-09-903-395-2
6	752.5	43.6	317	12	US-10-052-545-2
7	723	41.9	297	9	US-10-151-431-4
8	721	41.8	296	12	US-10-015-948-2
9	700	40.6	297	9	US-10-151-431-6
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13	358.5	20.8	364	10	US-09-731-030A-15
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35	312.5	18.1	321	9	US-10-146-065-2	Sequence 2, Appli
36	305.5	17.7	348	10	US-09-903-799-2	Sequence 2, Appli
37	305.5	17.7	353	10	US-09-771-063-2	Sequence 2, Appli
38	305.5	17.7	353	10	US-09-771-063-4	Sequence 4, Appli
39	305.5	17.7	353	12	US-10-037-616-23	Sequence 23, Appl
40	305	17.7	352	9	US-10-084-507B-21	Sequence 21, Appl
41	304.5	17.6	124	12	US-10-052-545-12	Sequence 12, Appl
42	304.5	17.6	353	9	US-10-084-507B-22	Sequence 22, Appl
43	304.5	17.6	353	10	US-09-731-030A-19	Sequence 19, Appl
44	304.5	17.6	354	10	US-09-879-225-2	Sequence 2, Appli
45	303.5	17.6	353	9	US-10-084-507B-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-09-884-211A-4  
; Sequence 4, Application US/09884211A  
; Publication No. US20030032791A1  
; GENERAL INFORMATION:  
; APPLICANT: Alan et. al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: PC10743A  
; CURRENT APPLICATION NUMBER: US/09/884,211A  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Canine MC4R protein Sequence  
US-09-884-211A-4

Query Match	100.0%	Score	1726;	DB	9;	Length	332;
Best Local Similarity	100.0%	Pred. No.	3.1e-149;				
Matches	332;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MNSTLQHGHTSLHFWNRSTYQGHGNATSLGKYPDGGCYEQLFVSPVFTLGVISLL	60				
Db	1	MNSTLQHGHTSLHFWNRSTYQGHGNATSLGKYPDGGCYEQLFVSPVFTLGVISLL	60				
Qy	61	ENILVIVAIANKNHLSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAOSFTVN	120				
Db	61	ENILVIVAIANKNHLSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAOSFTVN	120				
Qy	121	IDNWIDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRVGIIISCIWAACVTS	180				
Db	121	IDNWIDSVICSSLLASICSLLSIAVDYFTTFYALQYHNIMTVRVGIIISCIWAACVTS	180				
Qy	181	GILFTIYSDSTAVIICLTITMFTMLMALMASLYVHMFMLARLHIKRIAVLPGTGTROGAN	240				
Db	181	GILFTIYSDSTAVIICLTITMFTMLMALMASLYVHMFMLARLHIKRIAVLPGTGTROGAN	240				

Qy 241 MKGAIITLILGVVVCWAPFLLHLYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
Db 241 MKGAIITLILGVVVCWAPFLLHLYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332

RESULT 2

US-09-884-211A-3  
; Sequence 3, Application US/09884211A  
; Publication No. US20030032791A1  
; GENERAL INFORMATION:  
; APPLICANT: Alan et. al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: PC10743A  
; CURRENT APPLICATION NUMBER: US/09/884, 211A  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Feline MC4R protein Sequence  
US-09-884-211A-3

Query Match 97.6%; Score 1685; DB 9; Length 332;  
Best Local Similarity 97.6%; Pred. No. 1.6e-145;  
Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGGYDGGCYEQLFVSPFVTLGVISLL 60  
Db 1 MNSTLHGHGHTSLHFWNRSTYGOHGNATESLGGYDGGCYEQLFVSPFVTLGVISLL 60  
Qy 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120  
Db 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120  
Qy 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTIFALQYHNIMTVRRVGGIISCIWAACVTS 180  
Db 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTIFALQYHNIMTVRRVGGIISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GVLFIYSDSSAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240  
Qy 241 MKGAIITLILGVVVCWAPFLLHLYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
Db 241 MKGAIITLILGVVVCWAPFLLHLYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332

RESULT 3

US-09-910-180-2  
; Sequence 2, Application US/09910180  
; Publication No. US20030082678A1  
; GENERAL INFORMATION:  
; APPLICANT: Hsiung, Hansen  
; APPLICANT: Smith, Dennis  
; APPLICANT: Zhang, Xing-yue  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING BODY WEIGHT IN BOVINE SPE  
; FILE REFERENCE: P-12621  
; CURRENT APPLICATION NUMBER: US/09/910,180  
; CURRENT FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Bovine  
US-09-910-180-2  
Query Match 92.1%; Score 1590; DB 9; Length 332;  
Best Local Similarity 93.1%; Pred. No. 7.3e-137;  
Matches 309; Conservative 8; Mismatches 15; Indels 0; Gaps 0;  
Qy 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGGYDGGCYEQLFVSPFVTLGVISLL 60  
Db 1 MNSTQPLGHTSLHFWNRSAHGMPTNVSESLAKGYSDDGCEQLFVSPFVTLGVISLL 60  
Qy 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVN 120  
Db 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNGSETIVITLLNSTDDAQSFVD 120  
Qy 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTIFALQYHNIMTVRRVGGIISCIWAACVTS 180  
Db 121 IDNVDSVCSSLLASICSLSLSTAVDRYFTIFALQYHNIMTVRRVGGIISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GVLFIYSDSSAVIICLTIMFTMLALMASLYVHMFELMARLHKRIAVLPGTGTIRQGAN 240  
Qy 241 MKGAIITLILGVVVCWAPFLLHLYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
Db 241 MKGAIITLILGVVVCWAPFLLHLYISCPQNPYCVCFMSHFNLYLILMCSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332

RESULT 4

US-10-052-545-16  
; Sequence 16, Application US/10052545  
; Patent No. US20020142392A1  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/052,545  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,805  
; FILING DATE: 21-FEB-95  
; APPLICATION NUMBER: PCT/DK93/00273  
; FILING DATE: 20-AUG-93  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1046/92  
; FILING DATE: 21-AUG-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1118/92  
; FILING DATE: 10-SEP-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0528/93



Query Match	43.58;	Score	752.5;	DB	12;	Length	317;
Best Local Similarity	52.5%;	Pred. No.	1.1e-60;				
Matches	148;	Conservative	50;	Mismatches	81;	Indels	3;
Gaps	3;						
Qy	40	CYEQLFSPSEVFTLGLVISILENTLIVATAKKNLHSPMYFICSLAVADMLVSYNGS	99				
		: : :   : : :   : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
Db	35	CLE-VSISDGLFSLGLSVENALVYATAKRNHLHSPMYCFICCLALSDLLVSGSNVL	93				
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Qy	100	ETIVITLLNSTDDAQSTV-NIDNVDISVICSSLLASICSLSIADVRFYTFIYALQYH	158				
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Db	94	ETAVILLEGALVARAVLQQIDNVIDVTCSSMLSSLCFLGAIVADRIISIFYALRYH	153				
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Qy	159	NIMTVRRVGIISCIWAACACTVSGILFTIYSDSTAIVICLTITMFTMALMASIVVHFLM	218				
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Db	154	SIVTLPRARRVAAIWASVFTFLFAYVDHVAVLLCLVFFLAMLVLMAVLVYVHMLAR	213				
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Qy	219	ARLHIKRIAVL-PGTGTRIQQANMKGAITLITILIGVFWVCAPFFLHLFIYISCPQNPYC	277				
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Db	214	ACQHAQGIARLHKRPVHQGFGCLGAVALTILLGIFFLCWGPFELHLTIIVLCPEHPTC	273				
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Qy	278	VCPSMSHNLYLLIMCNSIIDPLIYALRSQELRKTKFEIICC	319				
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Db	274	GCFFKNFNFLAIIICNAIIDPLIYAFHSOELRRTLKEVLTC	315				
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Query Match      41.9%; Score 723; DB 9; Length 297;
Best Local Similarity 46.4%; Pred. No. 5e-58;
Matches 143; Conservative 57; Mismatches 90; Indels 18; Gaps 3;

QY      26 NATSLGKGYDGGCYEQLFVSPVEFVTLGVLSILENLIVATAKNKLNHSPMYFFICS 85
DB      6 NSYENINNARNNSDCPRVLUPEEIFFTSISVGVLENLIVLLAVFKNKLNQAPMYFFICS 65

QY      86 LAVADMVLVSVSGSETIVITLLNSTDDAQ--SFTVNIDNVDSVICSSLLASICSLLSIA 144
DB      66 LAISDMGLSLYKILENLIILRNWCYKLPGRSFETTADDIIDLFLVLSILGSIFSLSVIA 125

QY      145 VDRVETTFYALQYNIMTVRRVGIISCIWAACVTSGILFTIYSDSTAVIICLTIMFTFM 204
DB      126 ADVRTITFHALRYHSIVTMRRTVYLVLTIVTFTCTGTGTMVTFSHVHPVTIVTSLFPLM 185

QY      205 LALMASLYVHFMFLARLHIKRIAVLPGTGTTRQGNMKKGATLTLLIGVFVVCWAPFLH 264
DB      186 LVFILCYVHMFLLARSHTRKISTLP-----RANKMGATLTLLGVFFICWAPFLVH 238

QY      265 LIFVISCPOPCYVCFESHFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICYPLGG 324
DB      239 VLLMTFCPSNYCACYMSLFOVNGMLMCAVAIDPFYAFRSPPELDAFKKMTFC----- 293

QY      325 LCDLSRRY 332
DB      294 -----SRY 296

RESULT 8
US-10-015-948-2
; Sequence 2, Application US/10015948
; Patent No. US20020133843A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
; FILE OF INVENTION: ADRENOCORTICOTROPIN HORMONE RECEPTOR GENE DISRUPTIONS
; FILE REFERENCE: R-605
; CURRENT APPLICATION NUMBER: US/10/015,948
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,906
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/324,583
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-015-948-2

Query Match      41.8%; Score 721; DB 12; Length 296;
Best Local Similarity 48.3%; Pred. No. 7.5e-58;
Matches 144; Conservative 49; Mismatches 91; Indels 14; Gaps 3;

QY      23 QHGNALESKGYDPDGCYEQLFVSPVEFVTLGVLSILENLIVATAKNKLNHSPMYFF 82
DB      9 EHTNDTARNNSDCPD-----VVLPEEITFTTISVIGILENLIVLLAVTKNNLQSPMYFF 62

QY      83 ICSLAVADMVLVSVNGSETIVITLLNSTDDAQ--SFTVNIDNVDSVICSSLLASICSLL 141
DB      63 ICSLAISDMGLSLYKILENLIILRNWCYKLPGRSFETTADDIIDLFLVLSILGSIFSLS 122

QY      142 SIADVRYTFYALQYNIMTVRRVGIISCIWAACVTSGILFTIYSDSTAVIICLTIMF 201
DB      123 VIAADRYITTFHALQYHSIVTMRRTIITLIWNFCTGSGITWVTFSHIPTVLTFTSLF 182

QY      202 FTMALMASLYVHFMFLARLHIKRIAVLPGTGTTRQGNMKKGATLTLLIGVFVVCWAPF 261
DB      183 PLMLVFTLCIYIHMFLLARSHARISITLPT-----NNKGAMTLLIGVFICWAPF 235

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Qy 262 FLHLIFYSCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELRKTFFKEIICC 319  
Db 236 VLHVLLTFCPNPNYCVCMYSLFQVNGMLMNCNAVIDPFIYAFSPELRDAFKRMFLC 293

RESULT 9

US-10-151-431-6  
; Sequence 6, Application US/10151431  
; Publication No. US20030044973A1  
GENERAL INFORMATION:  
APPLICANT: Cone, Roger D  
Mountjoy, Kathleen G  
TITLE OF INVENTION: Mammalian Adrenocorticotrophic Hormone  
Receptors and Uses  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Allegrretti & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/151.431  
FILING DATE: 20-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/105.298  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/866.560  
FILING DATE: 10-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. US20030044973A1nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-151-431-6

Query Match 40.6%; Score 700; DB 9; Length 297;  
Best Local Similarity 49.6%; Pred. No. 6.2e-56;  
Matches .135; Conservative 47; Mismatches 82; Indels 8; Gaps 2;

Qy 49 EVFVTLGVISLLENILVIVAIKNNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLN 108  
Db 29 EIFTVSVIGVLENLWLVAVAKNLSQSPMYFFICSLAISDMGLSLYKILENVLMFKN 88  
Qy 109 STDTDAO-STVTNDNVIDSVICSSLLASICSLSIAVDVFTIFYALQVHNIMTVRRVG 167  
Db 89 MGYLEPGSFESTADDVDSVLISLGLSICSUSVIAADRYITIFHALQVHRIMTPAPCP 148  
Qy 168 IITSICWAACVSGILFIYSDSTAVIICLITFTFTMLMASLYVHMFLMARLHIKRIA 227  
Db 149 RHLTVLWAGTSGITIVTSHHVPVTALEPLMLAFILCYVHMFLMARSHTRTP 208  
Qy 228 VLPCTGTIROGANKMGKAITITILIGVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLY 287  
Db 209 SLP-----KANMRGAVTLTVLGVIFCWAPEVLHVLLMTFCPADPYCACYMSLFQVN 261

Qy 288 LILIMCNSIIDPLIYALRSQELRKTFFKEIICC 319  
Db 262 GVLMCNAIDPFIYAFSPELRYAFKRWVIC 293

RESULT 10

US-09-971-228-6  
; Sequence 6, Application US/09971228  
; Patent No. US20020155512A1  
GENERAL INFORMATION:  
APPLICANT: Liao, X. Charlene  
Masuda, Esteban  
APPLICANT: Chu, Peter  
APPLICANT: Pardo, Jorge  
APPLICANT: Li, Congfen  
APPLICANT: Zhao, Haoran  
APPLICANT: Jiang, Yingping  
APPLICANT: Rigel Pharmaceuticals, Incorporated  
TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration  
FILE REFERENCE: 021044-000310US  
CURRENT APPLICATION NUMBER: US/09/971.228  
CURRENT FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US 60/284,763  
PRIOR FILING DATE: 2001-04-18  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 364  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human endothelial differentiation G-protein  
OTHER INFORMATION: coupled receptor (GPCR) 2 (EDG2)  
US-09-971-228-6

Query Match 20.8%; Score 358.5; DB 9; Length 364;  
Best Local Similarity 28.4%; Pred. No. 9.3e-25;  
Matches 93; Conservative 67; Mismatches 113; Indels 55; Gaps 11;

Qy 15 FWRSTYQGH----GNATESLGKGYPDGGCYEQLFVSPVFTLVGIVSLLENILVIVAIA 70  
Db 33 FYNRS--GKHLATEWNTVSKLVMG-----LGITVCIFMLANLLVWVAIY 75  
Qy 71 KKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAOQSFVNIDNVDSVIC 130  
Db 76 VNRHFPIIYYLMANLAAADFFAGLA-----YFLMPTGNTRRLLTVTWLLRQGLID 129  
Qy 131 SLLASICSLSIAVDVFTIFYALQVHNIMTVRRVGIIISCIWAACVSGI----- 182  
Db 130 TSLTASVANLLAIAERHITVF-RMQLHTRMSNRVVVVIVITMAIVMGAIPSVGNHC 188  
Qy 183 -----LFIYSDSTAVIICLITFTFTMLMASLYVHMFLMARLHIKRIAVLPCTG 233  
Db 189 ICDIENGSNMPLYSDSYLVEWAFNL--VTFVWVVLVYAHIFGVYVQRTWRMS-RHSSG 245  
Qy 234 TIROGANKGAI-FLTILIGVVCWAPFFLHLIFYISCPQNPYCVG-FMSHFNLYLILI 291  
Db 246 PRRNRDTRMSLLKTVIVLGVAFIICWTFPLGLVLLLDVCCPO-----CDVLAYERFFLLLA 300  
Qy 292 MCNSIIDPLIYALRSQELRKTFFKEIICC 319  
Db 301 EFNSAMPIIYSYDRDKEMSATFROIICC 328

RESULT 11

US-09-811-838-2  
; Sequence 2, Application US/09811838  
; Publication No. US20030027800A1  
GENERAL INFORMATION:  
APPLICANT: Miller, Duane D.  
Tigyi, Gabor  
APPLICANT: Dalton, James T.



Db 189 ICDIENCSNAPLYSDSYLFWAIFNL--VTFVVMVLYAHIFGYVRQTRMS-RHSSG 245  
Qy 234 TIROGANMKGAI-TLTILIGVVFVVCWAPFFLHLIFYSQPNPCVC-FMSEHNLXLYLI 291  
Db 246 PRRNRTMMSLUKTVIVLGAFTICWTPGLVLLLDVCCPQ-----CDVLAYEKFELLLA 300  
Qy 292 MCNSIIDPLIYALRSQELRTFKKEIIC 319  
Db 301 EFNSAMNPIIYSYRDKEMSAFTRQILCC 328

## RESULT 14

US-10-037-616-20  
; Sequence 20, Application US/10037616  
; Patent No. US20020123148A1  
; GENERAL INFORMATION:  
; APPLICANT: English, Denis  
; APPLICANT: Kovacs, Richard J.  
; APPLICANT: Rizzo, Maria T.  
; APPLICANT: Sliva, Daniel T.  
; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use  
; FILE REFERENCE: 7042-119  
; CURRENT APPLICATION NUMBER: US/10/037,616  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/243,887  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-616-20

Query Match 20.8%; Score 358.5; DB 12; Length 364;  
Best Local Similarity 28.4%; Pred. No. 9.3e-25;  
Matches 93; Conservative 67; Mismatches 113; Indels 55; Gaps 11;  
Qy 15 FWNSTYGOH---GNATESLGKGYPDGGCYEQLFVSPFVTLGVISLLENILVIVAIA 70  
Db 33 FYNRS--GKHLATWNTVSKLVMG-----LGITVCIFIMLANLIVMAIY 75  
Qy 71 KKNLHSPMPYFFICSLAVADMLVSVNGSETIVITLLNSTDTDAQSFTNDNVDIVIC 130  
Db 76 VNRFRFPYIYLMANLAAADFEAGLA-----YFLMPTGPNTRRLTVSTWLLRQGLID 129  
Qy 131 SSLASICSLSIADRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTSGI----- 182  
Db 130 TSLTASVANLAIATERHITVF-RMQLHTRMSNRVVVIVVWMTAIVMGAIPSVGWN 188  
Qy 183 -----LFIYSDSTAVICILITMFFMLMASLYVHMFLMARLHKRIAVLPQTG 233  
Db 189 ICDIENCSNAPLYSDSYLFWAIFNL--VTFVVMVLYAHIFGYVRQTRMS-RHSSG 245  
Qy 234 TIROGANMKGAI-TLTILIGVVFVVCWAPFFLHLIFYSQPNPCVC-FMSEHNLXLYLI 291  
Db 246 PRRNRTMMSLUKTVIVLGAFTICWTPGLVLLLDVCCPQ-----CDVLAYEKFELLLA 300  
Qy 292 MCNSIIDPLIYALRSQELRTFKKEIIC 319  
Db 301 EFNSAMNPIIYSYRDKEMSAFTRQILCC 328

## RESULT 15

US-10-052-545-8  
; Sequence 8, Application US/10052545  
; Patent No. US20020142392A1  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/052,545  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,805  
; FILING DATE: 21-FEB-95  
; APPLICATION NUMBER: PCT/DK93/00273  
; FILING DATE: 20-AUG-93  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1046/92  
; FILING DATE: 21-AUG-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 1118/92  
; FILING DATE: 10-SEP-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0528/93  
; FILING DATE: 05-MAY-93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1102.0160000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 102 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
US-10-052-545-8

Query Match 19.2%; Score 332; DB 12; Length 102;  
Best Local Similarity 60.8%; Pred. No. 5.3e-21;  
Matches 62; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

Qy 152 FYALQYHNIMTVRRVGGIISCIWAACVTSGILFIYSDSTAVICILITMFFMLMASL 211  
Db 1 FYALRYHSIVTARRSGAIIAGIWAFCCTCGGIVFIFYSESTVYVILCLISNFFAMFLVSL 60  
Qy 212 YVHFMFLMARLHKRIAVLPQTGTIRQGANMKGAITLTILIGV 253  
Db 61 YIHMFLARTHVKRIALCPGPAIRGPGACRGAVTTLILGI 102

Search completed: June 4, 2003, 18:13:54  
Job time : 32 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 17:58:46 ; Search time 220.5 Seconds

(without alignments)  
970.755 Million cell updates/sec

Title: US-09-884-211A-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKETICCPGLGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

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- 24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*
- 25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*
- 26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*
- 27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1726	100.0	332	22	US-09-884-211A-4
2	1685	97.6	332	22	US-09-884-211A-3
3	1639.5	95.0	332	27	US-60-212-655-684
4	1638.5	94.9	332	6	US-08-200-711-8
5	1638.5	94.9	332	6	US-08-200-711B-8
6	1638.5	94.9	332	10	US-08-671-525A-8

Query Match	100.0%	Score	1726;	DB	22;	Length	332;
Best Local Similarity	100.0%	Pred. No.	2.5e-151;				
Matches	332;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKYPDGGCYEQLFVSPVFTLGVISLL	60				
Db	1	MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKYPDGGCYEQLFVSPVFTLGVISLL	60				

ALIGNMENTS

RESULT 1

US-09-884-211A-4  
; Sequence 4, Application US/09884211A  
; GENERAL INFORMATION:  
; APPLICANT: Alan et, al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: PC10743A  
; CURRENT APPLICATION NUMBER: US/09/884.211A  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Canine MC4R protein Sequence  
US-09-884-211A-4

Sequence 8, Appli  
Sequence 2, Appli  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 3, Appli  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
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Sequence 4, Appli  
Sequence 74, Appli  
Sequence 74, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
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Sequence 136, App  
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Sequence 4, Appli

QY 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180  
QY 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240  
Db 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240  
QY 241 MKGATITLILIGVVFVVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGATITLILIGVVFVVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
QY 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332  
Db 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332

## RESULT 2

US-09-884-211A-3  
; Sequence 3, Application US/09884211A  
; GENERAL INFORMATION:  
; APPLICANT: Alan et, al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: PC10743A  
; CURRENT APPLICATION NUMBER: US/09/884, 211A  
; PRIOR FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213, 909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Feline MC4R protein Sequence  
US-09-884-211A-3

Query Match 97.6%; Score 1685; DB 22; Length 332;  
Best Local Similarity 97.6%; Pred. No. 1.6e-147;  
Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60  
Db 1 MNSTLHGHHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60  
QY 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180  
QY 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240  
Db 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240  
QY 241 MKGATITLILIGVVFVVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGATITLILIGVVFVVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
QY 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332  
Db 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332

## RESULT 3

US-60-212-655-684

; Sequence 684, Application US/60212655  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL0000681  
; CURRENT APPLICATION NUMBER: US/60/212,655  
; NUMBER OF SEQ ID NOS: 1131  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 684  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-212-655-684

Query Match 95.0%; Score 1639.5; DB 27; Length 332;  
Best Local Similarity 95.8%; Pred. No. 2.7e-143;  
Matches 318; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYGOHGNATESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60  
Db 2 VNST-HRGHTSLHFWNRSSVRLHNSAESLGKGYDGGCYEQLEFVSPEVFTLGVISLL 60  
QY 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVAIAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASICSLLSIAVDRTFTFYALQYHNMVRRVGGIIISCIWAACVTS 180  
QY 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240  
Db 181 GILFIIYSDSTAVIICLTMTFMTLMALMASLVHMFMLARLHKRIAVLPGTGTIROGAN 240  
QY 241 MKGATITLILIGVVFVVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGATITLILIGVVFVVCWAPFHLIFVYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
QY 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332  
Db 301 IVALRSQELRKTFKEIICCPYLGGLCLSSRY 332

## RESULT 4

US-08-200-711-8  
; Sequence 8, Application US/08200711  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Harness, Dickey & Pierce  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/200,711  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F. 36683  
; REGISTRATION NUMBER:

TELEPHONE: (810)641-1600  
TELEFAX: (810)641-0270  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-671-525A-8

Query Match 94.9%; Score 1638.5; DB 10; Length 332;  
Best Local Similarity 95.5%; Pred. No. 3.4e-143;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGHMTSLHFWNRSTYGOHGNATESLKGYPDGGCYEQLFVSPVFTLGVISLL 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 VNST-HRGHMTSLHFWNRSSYRLHNSASESLKGYSDDGCGYEQLFVSPVFTLGVISLL 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVSVSNGSETIVITLLNSTDDTDAQSFTVN 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVSVSNGSETIIITLLNSTDDTDAQSFTVN 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFALQYHNIMTVRRVGGIIISCIWAACVTS 180  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVSVSNGSETIIITLLNSTDDTDAQSFTVN 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFALQYHNIMTVRRVGGIIISCIWAACVTS 180  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFALQYHNIMTVRRVGGIIISCIWAACVTS 180  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 181 GILFIYDSTAVIICLITMFTMLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 181 GILFIYDSSSAVVICLITMFTMLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 241 MKGAIITLTLIGVVFVVCWAPFFLHLFIYISCPONPYCVCFMSHFNLYLILIMCNSIIDPL 300  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 241 MKGAIITLTLIGVVFVVCWAPFFLHLFIYISCPONPYCVCFMSHFNLYLILIMCNSIIDPL 300  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

## RESULT 7

US-08-672-109A-8  
; Sequence 8, Application US/08672109A  
; GENERAL INFORMATION:  
; APPLICANT: Yanada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hartness, Dickey & Pierce  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,109A  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-00853  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270

INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-672-109A-8

Query Match 94.9%; Score 1638.5; DB 10; Length 332;  
Best Local Similarity 95.5%; Pred. No. 3.4e-143;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGHMTSLHFWNRSTYGOHGNATESLKGYPDGGCYEQLFVSPVFTLGVISLL 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 VNST-HRGHMTSLHFWNRSSYRLHNSASESLKGYSDDGCGYEQLFVSPVFTLGVISLL 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVSVSNGSETIVITLLNSTDDTDAQSFTVN 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVSVSNGSETIIITLLNSTDDTDAQSFTVN 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFALQYHNIMTVRRVGGIIISCIWAACVTS 180  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFALQYHNIMTVRRVGGIIISCIWAACVTS 180  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 181 GILFIYDSTAVIICLITMFTMLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 181 GILFIYDSSSAVVICLITMFTMLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 241 MKGAIITLTLIGVVFVVCWAPFFLHLFIYISCPONPYCVCFMSHFNLYLILIMCNSIIDPL 300  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 241 MKGAIITLTLIGVVFVVCWAPFFLHLFIYISCPONPYCVCFMSHFNLYLILIMCNSIIDPL 300  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 301 IYALRSQELRKTFKEIICCYPLGGCLDLSRY 332  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

## RESULT 8

US-08-780-749-2  
; Sequence 2, Application US/08780749  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank  
; APPLICANT: Huszar, Dennis  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS  
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/780,749  
; FILING DATE: 08-JAN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Laura A. Coruzzi  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-780-749-2

Query Match 94.9%; Score 1638.5; DB 11; Length 332;  
Best Local Similarity 95.5%; Pred. No. 3.4e-143;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;





Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTIROGAN 240  
Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTGTGAIROGAN 240  
Qy 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332

RESULT 14  
US-08-780-749-6  
: Sequence 6, Application US/08780749  
: GENERAL INFORMATION:  
: APPLICANT: Lee, Frank  
: APPLICANT: Huszar, Dennis  
: APPLICANT: Gu, Wei  
: TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS  
: TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Pennie & Edmonds LLP  
: STREET: 1155 Avenue of the Americas  
: CITY: New York  
: STATE: New York  
: COUNTRY: USA  
: ZIP: 10036/2711  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FastSeq Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/780,749  
: FILING DATE: 08-JAN-1997  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Laura A. Coruzzi  
: REGISTRATION NUMBER: 30,742  
: REFERENCE/DOCKET NUMBER: 7853-064  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (212) 790-9090  
: TELEFAX: (212) 869-8864/9741  
: TELEX: 66141 PENNIE  
: INFORMATION FOR SEQ ID NO: 6:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 332 amino acids  
: TYPE: amino acid  
: STRANDEDNESS:  
: TOPOLOGY: unknown  
: MOLECULE TYPE: protein  
US-08-780-749-6

Query Match 94.6%; Score 1632.5; DB 11; Length 332;  
Best Local Similarity 95.2%; Pred. No. 1.2e-142;  
Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;  
Qy 1 MNSTLQGHMTSLHFVNRSTYGOHGNATESLGKGYDPGCGYEQLFVSPVEFVTLGVISLL 60  
Db 2 VNST-HRGMHTSLHLNRRSYRLHSNASESLGKGYSDGCGYEQLFVSPVEFVTLGVISLL 60  
Qy 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Qy 121 IDNVDSVICSSLLASCSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASCSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTGTIROGAN 240  
Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTGTGAIROGAN 240  
Qy 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332

Search completed: June 4, 2003, 18:11:26  
Job time : 221.5 secs

Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTGTIROGAN 240  
Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTGTGAIROGAN 240  
Qy 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332

RESULT 15  
US-09-322-695-2  
: Sequence 2, Application US/09322695  
: GENERAL INFORMATION:  
: APPLICANT: Frank Lee  
: APPLICANT: Dennis Huszar  
: APPLICANT: Wei Gu  
: TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL  
: FILE REFERENCE: 7853-145  
: CURRENT APPLICATION NUMBER: US/09/322,695  
: CURRENT FILING DATE: 1999-05-28  
: EARLIER APPLICATION NUMBER: 08/662,560  
: EARLIER FILING DATE: 1996-06-10  
: NUMBER OF SEQ ID NOS: 12  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 2  
: LENGTH: 332  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-322-695-2

Query Match 94.6%; Score 1632.5; DB 17; Length 332;  
Best Local Similarity 95.2%; Pred. No. 1.2e-142;  
Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;  
Qy 1 MNSTLQGHMTSLHFVNRSTYGOHGNATESLGKGYDPGCGYEQLFVSPVEFVTLGVISLL 60  
Db 2 VNST-HRGMHTSLHLNRRSYRLHSNASESLGKGYSDGCGYEQLFVSPVEFVTLGVISLL 60  
Qy 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Db 61 ENILVIVAIKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120  
Qy 121 IDNVDSVICSSLLASCSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASCSLLSIADRYFTIFYALQYHNIMTVRRVGIISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTGTIROGAN 240  
Db 181 GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLMARLHIKRIAVLPCTGTGTGAIROGAN 240  
Qy 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAITITILIGVFWCWAPFFLHIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGCLDLSSRY 332

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:01:21 ; Search time 36 seconds  
(without alignments)  
1944.050 Million cell updates/sec

Title: US-09-884-211A-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFNWRSST.....FKETICCYPLGGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006677 seqs, 210800627 residues

Total number of hits satisfying chosen parameters: 1006677

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pap:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pap:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pap:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pap:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pap:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pap:\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1639.5	95.0	332	7	US-60-443-566-3564
2	1639.5	95.0	332	7	US-60-452-680-13557
3	1639.5	95.0	332	7	US-60-455-444-4680
4	1639.5	95.0	332	7	US-60-465-241-4680
5	1638.5	94.9	332	6	US-10-225-567A-158
6	1638.5	94.9	332	6	US-10-414-521-1
7	1638.5	94.9	332	6	US-10-318-661-27
8	1632.5	94.6	332	6	US-10-413-752-2
9	1624.5	94.1	332	6	US-10-373-355-2
10	1624.5	94.1	332	6	US-60-427-882-2
11	1620.5	93.9	332	6	US-10-413-752-6
12	1592.5	92.3	332	6	US-10-288-160-16
13	1463	84.8	311	5	US-09-380-419C-3
14	1257	72.8	248	5	US-09-380-419C-4
15	1026.5	59.4	325	6	US-10-288-160-18
16	1025.5	59.4	325	1	PCT-US03-04816-40
17	1025.5	59.4	325	5	US-09-831-228-2
18	1025.5	59.4	325	6	US-10-225-567A-160
19	1025.5	59.4	325	6	US-10-369-022-40
20	982.5	56.9	360	5	US-09-949-004-341
21	982.5	56.9	360	6	US-10-219-051B-9975
22	982.5	56.9	360	7	US-60-452-680-13621
23	982.5	56.9	360	7	US-60-453-135-8500
24	982.5	56.9	360	7	US-60-453-050-8500
25	982.5	56.9	360	7	US-60-466-412-8500
26	981.5	56.9	360	5	US-09-949-004-302

ALIGNMENTS

RESULT 1

US-60-443-566-3564

; Sequence 3564, Application US/60443566

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: BEGOVICH, Ann

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001447

; CURRENT APPLICATION NUMBER: US/60/443,566

; NUMBER OF SEQ ID NOS: 25102

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3564

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-60-443-566-3564

Query Match

Best Local Similarity 95.0%; Score 1639.5; DB 7; Length 332;

Matches 316; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy	1	MNSTLQHGHTSLHFNWRSSTYGQHGHNATESLGKGYPDGCGCYEQLFVSPVFTLGVISLL	60
Db	2	VNST-HRGMHTSLHLNRRSSYRLHNSASESLGKGYSDGCGCYEQLFVSPVFTLGVISLL	60
Qy	61	ENILVIVAIANKNLHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN	120
Db	61	ENILVIVAIANKNLHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN	120
Qy	121	IDNVDSVCSSLASICSLSIAVDRTFFYALQYHNIMTVRRVGIISCIWAACVTS	180
Db	121	IDNVDSVCSSLASICSLSIAVDRTFFYALQYHNIMTVRRVGIISCIWAACVTS	180
Qy	181	GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLARLHKRIAVLPCTGTROGAN	240
Db	181	GILFIYSDSTAVIICLITMFTMALMASLYVHMFMLARLHKRIAVLPCTGTROGAN	240
Qy	241	MKGATITLIGVFWCVWAPFFLHIFVISCQPNPCVCFMSHFNLYLILIMCNSIIDPL	300
Db	241	MKGATITLIGVFWCVWAPFFLHIFVISCQPNPCVCFMSHFNLYLILIMCNSIIDPL	300
Qy	301	IYALRSQELRKTFFKEIICCCYPLGGLDLSRY	332
Db	301	IYALRSQELRKTFFKEIICCCYPLGGLDLSRY	332

RESULT 2

US-60-452-680-13557

; Sequence 13557, Application US/60452680

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: GRUPE, Andrew

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT FILING DATE: 2003-03-07

; NUMBER OF SEQ ID NOS: 116213

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13557

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

US-60-452-680-13557

Query Match 95.0%; Score 1639.5; DB 7; Length 332;

Best Local Similarity 95.8%; Pred. No. 1e-153;

Matches 318; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYBOLFVSPEVFTLGVISLL 60

Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYSDGCGYBOLFVSPEVFTLGVISLL 60

QY 61 ENILVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

Db 61 ENILVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

QY 121 INVIDSVTCSSLLASICSLLSIADVDYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

Db 121 INVIDSVTCSSLLASICSLLSIADVDYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

QY 241 MKGAIITLTILIGVVFVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILMCSIIDPL 300

Db 241 MKGAIITLTILIGVVFVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILMCSIIDPL 300

QY 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSRY 332

Db 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSRY 332

RESULT 3

US-60-455-444-4680

; Sequence 4680, Application US/60455444

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: BEGOVICH, Ann

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

; CURRENT FILING DATE: 2003-03-18

; NUMBER OF SEQ ID NOS: 50986

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4680

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

US-60-455-444-4680

Query Match 95.0%; Score 1639.5; DB 7; Length 332;

Best Local Similarity 95.8%; Pred. No. 1e-153;

Matches 318; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYBOLFVSPEVFTLGVISLL 60

Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYSDGCGYBOLFVSPEVFTLGVISLL 60

QY 61 ENILVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

Db 61 ENILVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

QY 121 INVIDSVTCSSLLASICSLLSIADVDYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

Db 121 INVIDSVTCSSLLASICSLLSIADVDYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

QY 241 MKGAIITLTILIGVVFVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILMCSIIDPL 300

Db 241 MKGAIITLTILIGVVFVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILMCSIIDPL 300

QY 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSRY 332

Db 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSRY 332

RESULT 4

US-60-465-241-4680

; Sequence 4680, Application US/60465241

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: BEGOVICH, Ann

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

; CURRENT FILING DATE: 2003-04-23

; NUMBER OF SEQ ID NOS: 258418

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4680

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

US-60-465-241-4680

Query Match 95.0%; Score 1639.5; DB 7; Length 332;

Best Local Similarity 95.8%; Pred. No. 1e-153;

Matches 318; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYBOLFVSPEVFTLGVISLL 60

Db 2 VNST-HRGMHTSLHLWNRSSYRLHNSASESLGKGYSDGCGYBOLFVSPEVFTLGVISLL 60

QY 61 ENILVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

Db 61 ENILVIAIAKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

QY 121 INVIDSVTCSSLLASICSLLSIADVDYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

Db 121 INVIDSVTCSSLLASICSLLSIADVDYFTFYALQYHNMVRRVGGIISCIWAACVTS 180

QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLYVHMFMLARLHKRIAVLPGTGTIRQGAN 240

QY 241 MKGAIITLTILIGVVFVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILMCSIIDPL 300

Db 241 MKGAIITLTILIGVVFVVCWAPFFLHLFIYISCPQNPYCVCFMSHFENLYLILMCSIIDPL 300

QY 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSRY 332

Db 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSRY 332

RESULT 5

US-10-225-567A-158

; Sequence 158, Application US/10225567A

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; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 158
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-158

Query Match          94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 1.3e-153;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGMHTSLHFNWRSYTGQGNATSLGKGYPDGGCYEQLFVSPVFTLGVISLL 60
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLNRRSSYRLHSNASESLGRKGYSDGGCYEQLFVSPVFTLGVISLL 60
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 121 IDNVDSVICSLLASCSLLSIADVRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 121 IDNVDSVICSLLASCSLLSIADVRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 181 GILFIYSDSTAVIICLITMFFTMLMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLITMFFTMLMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 241 MKGAIITLILGVVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 241 MKGAIITLILGVVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 301 IYALRSQELRKTKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 301 IYALRSQELRKTKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-10-414-521-1
; Sequence 1, Application US/10414521
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Colson, Anny-Odile
; APPLICANT: Mieling, Glen
; TITLE OF INVENTION: Three Dimensional Coordinates of Melanocortin-4 Receptors
; FILE REFERENCE: 9207
; CURRENT APPLICATION NUMBER: US/10/414,521
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-414-521-1

Query Match          94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 1.3e-153;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGMHTSLHFNWRSYTGQGNATSLGKGYPDGGCYEQLFVSPVFTLGVISLL 60
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
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Db 2 VNST-HRGMHTSLHLNRRSSYRLHSNASESLGRKGYSDGGCYEQLFVSPVFTLGVISLL 60
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 121 IDNVDSVICSLLASCSLLSIADVRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 121 IDNVDSVICSLLASCSLLSIADVRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 181 GILFIYSDSTAVIICLITMFFTMLMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLITMFFTMLMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 241 MKGAIITLILGVVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 241 MKGAIITLILGVVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 301 IYALRSQELRKTKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 301 IYALRSQELRKTKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-318-661-27
; Sequence 27, Application US/10318661
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Synthesized By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-27

Query Match          94.9%; Score 1638.5; DB 6; Length 332;
Best Local Similarity 95.5%; Pred. No. 1.3e-153;
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQGMHTSLHFNWRSYTGQGNATSLGKGYPDGGCYEQLFVSPVFTLGVISLL 60
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 2 VNST-HRGMHTSLHLNRRSSYRLHSNASESLGRKGYSDGGCYEQLFVSPVFTLGVISLL 60
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVSNGSETIVITLLNSTDTDAQSFTVN 120
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 121 IDNVDSVICSLLASCSLLSIADVRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 121 IDNVDSVICSLLASCSLLSIADVRYFTFYALQYHNIMTVRRVGIISCIWAACVTS 180
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 181 GILFIYSDSTAVIICLITMFFTMLMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 181 GILFIYSDSTAVIICLITMFFTMLMASLYVHMFMLMARLHKRIKRIAVLPCTGTIROGAN 240
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 241 MKGAIITLILGVVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
Db 241 MKGAIITLILGVVVCWAPFFLHLIFYISCPNPYCVCFMSHFNLYLILIMCNSIIDPL 300
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
QY 301 IYALRSQELRKTKEIICCCYPLGGLCDLSSRY 332
   :||| ||||| ||||| : ||:||||| ||||| ||||| ||||| ||||| |||||
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Db 301 IYALRSQELRKTKEIIICYPGLGCLDLSRY 332  
RESULT 8  
US-10-413-752-2  
; Sequence 2, Application US/10413752  
; GENERAL INFORMATION:  
; APPLICANT: Frank Lee  
; APPLICANT: Dennis Huszar  
; APPLICANT: Wei Gu  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL  
; TITLE OF INVENTION: IN THE REGULATION OF BODY WEIGHT  
; FILE REFERENCE: 7853-145  
; CURRENT APPLICATION NUMBER: US/10/413,752  
; CURRENT FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: US/09/322,695  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 08/662,560  
; PRIOR FILING DATE: 1996-06-10  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-413-752-2

Query Match 94.6%; Score 1632.5; DB 6; Length 332;  
Best Local Similarity 95.2%; Pred. No. 5.1e-153;  
Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;  
QY 1 MNSTLQHGHTSLHFWNRSTYQGHGNATESLGKGYPDGGCYEQLFVSPVFTLVGISLL 60  
Db 2 VNST-HRGMHTSLHFWNRSTYQGHGNATESLGKGYSDGGCYEQLFVSPVFTLVGISLL 60  
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDDAQSFVN 120  
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDDAQSFVN 120  
QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
QY 181 GILFIYSDSTAVIICLTMTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GILFIYSDSTAVIICLTMTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
QY 181 GILFIYSDSTAVIICLTMTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GILFIYSDSTAVIICLTMTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
QY 241 MKGATLTILIGVVCWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
Db 241 MKGATLTILIGVVCWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
QY 301 IYALRSQELRKTKEIIICYPGLGCLDLSRY 332  
Db 301 IYALRSQELRKTKEIIICYPGLGCLDLSRY 332

RESULT 9  
US-10-373-355-2  
; Sequence 2, Application US/10373355  
; GENERAL INFORMATION:  
; APPLICANT: MacNeill, Douglas J.  
; APPLICANT: Weinberg, David H.  
; APPLICANT: Van der Ploeg, Leonardus H. T.  
; TITLE OF INVENTION: DNA MOLECULES ENCODING THE MELANOCORTIN  
; TITLE OF INVENTION: 4 RECEPTOR PROTEIN FROM RHESUS MONKEY  
; FILE REFERENCE: 20190P  
; CURRENT APPLICATION NUMBER: US/10/373,355  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: US/09/831,206  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: PCT/US99/25767  
; PRIOR FILING DATE: 1999-11-05

; PRIOR APPLICATION NUMBER: 60/107,721  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: rhesus monkey (Macaca mulatta)  
US-10-373-355-2  
Query Match 94.1%; Score 1624.5; DB 6; Length 332;  
Best Local Similarity 94.6%; Pred. No. 3.1e-152;  
Matches 314; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
QY 1 MNSTLQHGHTSLHFWNRSTYQGHGNATESLGKGYPDGGCYEQLFVSPVFTLVGISLL 60  
Db 2 VNST-HRGMHTSLHFWNRSTYQGHGNATESLGKGYSDGGCYEQLFVSPVFTLVGISLL 60  
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDDAQSFVN 120  
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDDAQSFVN 120  
QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
QY 181 GILFIYSDSTAVIICLTMTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GILFIYSDSTAVIICLTMTMLALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
QY 241 MKGATLTILIGVVCWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
Db 241 MKGATLTILIGVVCWAPFHLHFIYISCPQNPYCVCFMSHFNLYLILMNCNSIIDPL 300  
QY 301 IYALRSQELRKTKEIIICYPGLGCLDLSRY 332  
Db 301 IYALRSQELRKTKEIIICYPGLGCLDLSRY 332  
RESULT 10  
US-60-427-882-2  
; Sequence 2, Application US/60427882  
; GENERAL INFORMATION:  
; APPLICANT: Boss, Olivier Dominique  
; APPLICANT: Coirier, Albane  
; TITLE OF INVENTION: Melanocortin receptor MC4-R  
; FILE REFERENCE: 4-32767 P1  
; CURRENT APPLICATION NUMBER: US/60/427,882  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Cynomolgus Monkey  
US-60-427-882-2  
Query Match 94.1%; Score 1624.5; DB 7; Length 332;  
Best Local Similarity 94.6%; Pred. No. 3.1e-152;  
Matches 314; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
QY 1 MNSTLQHGHTSLHFWNRSTYQGHGNATESLGKGYPDGGCYEQLFVSPVFTLVGISLL 60  
Db 2 VNST-HRGMHTSLHFWNRSTYQGHGNATESLGKGYSDGGCYEQLFVSPVFTLVGISLL 60  
QY 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDDAQSFVN 120  
Db 61 ENILVIVAIAKKNLHSPMYFFICSLAVADMVSVNSGSETIVITLLNSTDDAQSFVN 120  
QY 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASICSLLSIADVRYFTIFYALQYHNIMTVRRVGGIISCIWAACVTS 180

Qy 181 GILFIYSDTAVIICLITMFTMLMASLYVHMFMLARLHKRIAVLPCTGTIROGAN 240  
Db 181 GILFIYSDSAVILICLITMFTMLMASLYVHMFMLARLHKRIAVLPCTGAIRQGAN 240  
Qy 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSVIDPL 300  
Qy 301 IYALRSQELRKTKEIKICCYPLGGLCDLSRY 332  
Db 301 IYALRSQELRKTKEIKICCYPLGGLCDLSRY 332

RESULT 11  
US-10-413-752-6  
Sequence 6, Application US/10413752  
GENERAL INFORMATION:  
APPLICANT: Frank Lee  
APPLICANT: Dennis Huszar  
APPLICANT: Wei Gu  
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL  
IN THE REGULATION OF BODY WEIGHT  
FILE REFERENCE: 7953-145  
CURRENT APPLICATION NUMBER: US/10/413,752  
PRIOR FILING DATE: 2003-04-14  
PRIOR APPLICATION NUMBER: US/09/322,695  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 08/662,560  
PRIOR FILING DATE: 1996-06-10  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 332  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-10-413-752-6

Query Match 93.9%; Score 1620.5; DB 6; Length 332;  
Best Local Similarity 94.3%; Pred. No. 7.8e-152;  
Matches 313; Conservative 7; Mismatches 11; Indels 1; Gaps 1;  
Qy 1 MNSTLQHGHTSLHFNWNRSTYGOHGNATESLGKYPDGGCYEQLFVSPVEVFTLGVISLL 60  
Db 2 VNST-HRGMHTSLHLNWRSSVRLHNSASESLGKYSDBGCYEQLFVSPVEVFTLGVISLL 60  
Qy 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSTFVN 120  
Db 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSTFVN 120  
Qy 121 IDNVDSVICSSLLASCSLLSIADVRYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASCSLLSIADVRYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180  
Qy 181 GILFIYSDTAVIICLITMFTMLMASLYVHMFMLARLHKRIAVLPCTGTIROGAN 240  
Db 181 GVLFIYSDSAVILICLITMFTMLMASLYVHMFMLARLHKRIAVLPCTGAIRQGAN 240  
Qy 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSVIDPL 300  
Qy 301 IYALRSQELRKTKEIKICCYPLGGLCDLSRY 332  
Db 301 IYALRSQELRKTKEIKICCYPLGGLCDLSRY 332

RESULT 12  
US-10-288-160-16  
Sequence 16, Application US/10288160  
GENERAL INFORMATION:  
APPLICANT: Cone, Roger D  
Fan, Wei  
Boston, Bruce A

Kesterton, Robert A  
Lu, Dongsi  
Chen, Wenbiao  
TITLE OF INVENTION: Methods and Reagents for Discovering and  
Using Mammalian Melanocortin Receptor Agonists and Antag  
To Modulate Feeding Behavior in Animals  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/288,160  
FILING DATE: 05-Nov-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,281  
FILING DATE: 04-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Noonan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 96,886  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-288-160-16  
Query Match 92.3%; Score 1592.5; DB 6; Length 332;  
Best Local Similarity 93.4%; Pred. No. 4.6e-149;  
Matches 310; Conservative 7; Mismatches 14; Indels 1; Gaps 1;  
Qy 1 MNSTLQHGHTSLHFNWNRSTYGOHGNATESLGKYPDGGCYEQLFVSPVEVFTLGVISLL 60  
Db 2 VNST-HRGMHTSLHLNWRSSVRLHNSASESLGKYSDBGCYEQLFVSPVEVFTLGVISLL 60  
Qy 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSTFVN 120  
Db 61 ENILVIVAIAKNNLHSPMYFFTCISLAVADMLVSVNSGSETIVITLLNSTDTDAQSTFVN 120  
Qy 121 IDNVDSVICSSLLASCSLLSIADVRYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSSLLASCSLLSIADVRYFTIFYALQYHNMTVRRVGIIISCIWAACVTS 180  
Qy 181 GILFIYSDTAVIICLITMFTMLMASLYVHMFMLARLHKRIAVLPCTGTIROGAN 240  
Db 181 GILFIYSDSAVILICLITMFTMLMASLYVHMFMLARLHKRIAVLPCTGAIRQGAN 240  
Qy 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Db 241 MKGAIITLILIGVFWCWAPFFLHLIFYISCPQNPYCVCFMSHFNLYLILIMCNSIIDPL 300  
Qy 301 IYALRSQELRKTKEIKICCYPLGGLCDLSRY 332  
Db 301 IYALRSQELRKTKEIKICCYPLGGLCDLSRY 332  
RESULT 13

US-09-380-419C-3  
; Sequence 3, Application US/09380419C  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max F.  
; APPLICANT: Larsen, Neils  
; APPLICANT: Kim, Kwan  
; TITLE OF INVENTION: Melanocortin-4 Receptor Gene and Use as a Genetic Marker for Fat  
; FILE OF INVENTION: Weight Gain, and/or Feed Consumption in Animals  
; FILE REFERENCE: ISURF 2413  
; CURRENT APPLICATION NUMBER: US/09/380,419C  
; CURRENT FILING DATE: 2000-07-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 311  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (298)..(298)  
; OTHER INFORMATION: "X" can be any amino acid  
US-09-380-419C-3

Query Match 84.8%; Score 1463; DB 5; Length 311;  
Best Local Similarity 98.3%; Pred. No. 2.6e-136;  
Matches 285; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 43 QLFVSPVFTVLGVISLLENILVIVAIAKKNLHSPMYFFICSLAVADMVSVSNGSETI 102  
Db 1 QLFVSPVFTVLGVISLLENILVIVAIAKKNLHSPMYFFICSLAVADMVSVSNGSETI 60  
QY 103 VITLLNSTDTDAQSFVNIDNVIDSVICSSLLASICSLSIAVDRVFTIFYALQYHNMT 162  
Db 61 IITLLNSTDTDAQSFVNIDNVIDSVICSSLLASICSLSIAVDRVFTIFYALQYHNMT 120  
QY 163 VRVGTIIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFMLARLH 222  
Db 121 VRVGTIIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFMLARLH 180  
QY 223 IKRIAVLPGTGIRQGANMKGAITLTILIGVFVVCWAPFHLHIFYISCPQNPYCVCFMS 282  
Db 181 IKRIAVLPGTGIRQGANMKGAITLTILIGVFVVCWAPFHLHIFYISCPQNPYCVCFMS 240  
QY 283 HFNLYLILMCSNIIDPLIYALRSQELRTFKFKEICCYPLGGCLDLSRY 332  
Db 241 HFNLYLILMCSNIIDPLIYALRSQELRTFKFKEICCYPLGGCLDLSRY 290

RESULT 14  
US-09-380-419C-4  
; Sequence 4, Application US/09380419C  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max F.  
; APPLICANT: Larsen, Neils  
; APPLICANT: Kim, Kwan  
; TITLE OF INVENTION: Melanocortin-4 Receptor Gene and Use as a Genetic Marker for Fat  
; FILE OF INVENTION: Weight Gain, and/or Feed Consumption in Animals  
; FILE REFERENCE: ISURF 2413  
; CURRENT APPLICATION NUMBER: US/09/380,419C  
; CURRENT FILING DATE: 2000-07-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-380-419C-4

Query Match 72.8%; Score 1257; DB 5; Length 248;  
Best Local Similarity 97.6%; Pred. No. 4.5e-116;  
Matches 242; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 73 KNLHSPMYFFICSLAVADMVSVSNGSETIVITLLNSTDTDAQSFVNIDNVIDSVICSS 132

Db 1 KNLHSPMYFFICSLAVADMVSVSNGSETIVITLLNSTDTDAQSFVNIDNVIDSVICSS 60  
QY 133 LLASICSLSIAVDRVFTIFYALQYHNMTVRVGTIIISCIWAACVSGILFTIYSDSTA 192  
Db 61 LLASICSLSIAVDRVFTIFYALQYHNMTVRVGTIIISCIWAACVSGILFTIYSDSTA 120  
QY 193 VIICLTMTFTMLMASLYVHMFMLARLHMKRIAVLPGTGIRQGANMKGAITLTILIG 252  
Db 121 VIICLTMTFTMLMASLYVHMFMLARLHMKRIAVLPGTGIRQGANMKGAITLTILIG 180  
QY 253 VFVVCWAPFHLHIFYISCPQNPYCVCFMSHFNLYLILMCSNIIDPLIYALRSQELRT 312  
Db 181 VFVVCWAPFHLHIFYISCPQNPYCVCFMSHFNLYLILMCSNIIDPLIYALRSQELRT 240  
QY 313 FREIICCY 320  
Db 241 FREIICCY 248

RESULT 15

US-10-288-160-18  
; Sequence 18, Application US/10288160  
; GENERAL INFORMATION:  
; APPLICANT: Cone, Roger D  
; APPLICANT: Fan, Wei  
; APPLICANT: Boston, Bruce A  
; APPLICANT: Kesterton, Robert A  
; APPLICANT: Lu, Dongsi  
; APPLICANT: Chen, Wenbiao

TITLE OF INVENTION: Methods and Reagents for Discovering and  
Using Mammalian Melanocortin Receptor Agonists and Antag  
To Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/288,160  
FILING DATE: 05-Nov-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,281  
FILING DATE: 04-SEP-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Noonan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 96,886  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-288-160-18  
Query Match 59.5%; Score 1026.5; DB 6; Length 325;  
Best Local Similarity 66.8%; Pred. No. 3.9e-93;  
Matches 195; Conservative 43; Mismatches 53; Indels 1; Gaps 1;

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Qy 42 EQLFVSEVFTLGVISLLENILVIVAIAKNKNLHSPMYFFICSLAVADMLVSVNGSET 101
Db 34 EEMGIAVEVELTGLVSLLENILVIGAIVKNKNLHSPMYFVGSLAVADMLVSMNAWET 93
Qy 102 IVITLLNSTD-TDAQSFVNIDNVDSVICSSLLASTCSLSIAVDRYFTIFYALQYHNI 160
Db 94 VTIYLLNKNKHLVIADTFVRHIDNVFDSMICISVVASMCSSLIAIAVDRYITIFYALRYHHI 153
Qy 161 MTVRRVGIILSCIAWAACTVSGILFIYISDSTAVIICLIITWFFTMALMASLYVHMFILMAR 220
Db 154 MTARRSGVLIACIWTFCISGIVFIYIESKYVICLIISMFFTMLFFMVSLYIHMFLIAR 213
Qy 221 LHIKRIAVLPGTGTIRQCANNKGAITLTILIGVVCWAPFFLHLIFYISCPQNPYCVCF 280
Db 214 NHVKRIAASPRYNSVRQRTSMKGAITLTMLLGIFIVCWSPEFFLHLIIMISCPQNPYCSF 273
Qy 281 MSHFNLYLILIMCNSIIDPLIYALRSQELRKTEIICCYPLGGLCDLSRY 332
Db 274 MSYFNMYLILIMCNSVIDPLIYALRSQEMRTEKEIVCCHGFRRCRLGGY 325

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Search completed: June 4, 2003, 18:12:46  
Job time : 37 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 18:12:51 ; Search time 26 seconds  
(without alignments)  
1227.563 Million cell updates/sec

Title: US-09-884-211a-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKETICYPGLGGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1632.5	94.6	332	2 A57055	melanocortin recep
2	1070	62.0	215	2 B57055	melanocortin-4 rec
3	1041	60.3	325	2 JC2193	melanocortin recep
4	1023.5	59.3	372	2 I49008	melanocortin-5 rec
5	1022.5	59.2	325	2 JC5592	melanocortin 5 rec
6	1003.5	58.1	325	2 JN0764	melanocortin recep
7	994	57.6	323	2 S43850	melanocortin 3 rec
8	987.5	57.2	360	2 B46647	melanocortin recep
9	965	55.9	323	2 S36636	melanocortin recep
10	962.5	55.8	325	2 I46416	melanocyte-stimula
11	830.5	48.1	314	2 S71420	melanocortin 1 rec
12	817.5	47.4	314	2 S70005	melanocortin 1 rec
13	770	44.6	317	2 S45708	MSH receptor - bov
14	766	44.4	317	2 T12055	melanocyte stimula
15	752.5	43.6	315	2 S25581	melanocyte-stimula
16	751.5	43.5	317	2 S29204	melanocortin recep
17	724	41.9	297	2 S42767	adrenocorticotropi
18	723	41.9	297	2 C43265	adrenocorticotropi
19	721	41.8	296	2 I52326	adrenocorticotropi
20	718	41.6	296	2 JC4046	adrenocorticotropi
21	700	40.6	297	2 I45849	gene ACTH receptor
22	358.5	20.8	364	2 JC5293	lysophosphatidic a
23	329.5	19.1	383	2 I53870	Egfr-1 orphan recep
24	327	18.9	362	2 JC7559	sphingosine 1-phos
25	323	18.7	317	2 JC2335	melanocortin recep
26	320.5	18.6	381	2 A35300	G protein-coupled
27	316.5	18.3	330	2 A55689	G protein-coupled
28	305	17.7	352	2 JC1465	probable G protein
29	302.5	17.5	330	2 S40454	G protein-coupled

#### RESULT 1

A57055

melanocortin receptor 4 - human

C:Species: Homo sapiens (man)

C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 24-Sep-1999

C:Accession: A57055; A47111

R:Mountjoy, K.G.; Mortrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.

Mol. Endocrinol. 8, 1298-1308, 1994

A:Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and au

A:Reference number: A57055; MUID:95157557; PMID:7854347

A:Accession: A57055

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-332 <MOU>

A:Cross-references: GB:S77415; NID:g998456; PIDN:AA33341.1; PID:g998457

R:Gantz, I.; Miwa, H.; Konda, Y.; Shimoto, Y.; Tashiro, T.; Watson, S.J.; DelValle, J

J. Biol. Chem. 268, 15174-15179, 1993

A:Title: Molecular cloning, expression, and gene localization of a fourth melanocorti

A:Reference number: A47111; MUID:93315499; PMID:8392067

A:Accession: A47111

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-168, 'I', 170-332 <GAN>

A:Cross-references: GB:L08603; NID:g291977; PIDN:AAA35791.1; PID:g291978

C:Genetics:

A:Gene: GDB:MC4R

A:Cross-references: GDB:203939; OMIM:155541

A:Map position: 20q13.2-20q13.3

C:Superfamily: melanocortin receptor

C:Keywords: hormone receptor

Query Match 94.6%; Score 1632.5; DB 2; Length 332;

Best Local Similarity 95.2%; Pred. No. 3.3e-126;

Matches 316; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYPDGCGYEQLFVSPVEVFTLGVISLL 60

Db 2 VNST-HRGMTTSLHWNRSYRLHNSASESLGKGYSDGCGYEQLFVSPVEVFTLGVISLL 60

Qy 61 ENILVIVAIARKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFIVN 120

Db 61 ENILVIVAIARKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFIVN 120

Qy 121 IDNVDSVICSLLASICSLLSIADVRYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Db 121 IDNVDSVICSLLASICSLLSIADVRYFTTFYALQYHNIMTVRRVGIISCIWAACVTS 180

Qy 181 GILFIYSDTAVIICLITMFFTMALMASLYVMFLMARLHRIKRIAVLPCTGTGIRGAN 240

Db 181 GILFIYSDSAVICLITMFFTMALMASLYVMFLMARLHRIKRIAVLPCTGTGIRGAN 240

Qy 241 MKGAIITLILGVFVVCWAPFFLLHIFVISCQPONPYCVCFMSHENLVILIMCNSIIDPL 300

#### ALIGNMENTS

Db 241 MKGAITLTILIGVFWVWAPFFHFLFYISCPNYPVCVCFMSHFNLYLILMCSNIDPL 300  
QY 301 IYALRSQELRKTKEIKICCPYGLGCLDLSSRY 332  
Db 301 IYALRSQELRKTKEIKICCPYGLGCLDLSSRY 332  
RESULT 2  
B57055  
melanocortin-4 receptor - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 07-May-1999  
C:Accession: B57055  
R:Mountjoy, K.G.; Mordrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.  
Mol. Endocrinol. 8, 1298-1308, 1994  
A:Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and autonomic nervous system of the rat.  
A:Reference number: A57055; MUID:95157557; PMID:7854347  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-215 <MOU>  
C:Superfamily: melanocortin receptor

Query Match 62.0%; Score 1070; DB 2; Length 215;  
Best Local Similarity 96.3%; Pred. No. 2.3e-80;  
Matches 207; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
QY 78 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSFVNIDNVIDSVICSSLLASI 137  
Db 1 PMYFFICSLAVADMLVSVNGSETIVITLLNSTDDAQSFVNIDNVIDSVICSSLLASI 60  
QY 138 CSLLSTAVDRYFTIFAYALQYHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICL 197  
Db 61 CSLLSTAVDRYFTIFAYALQYHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICL 120  
QY 198 ITMFFMLALMASLYVHMFMLARLHKRIAVLPCTGTIRQANMKMGATITLILIGVFWVC 257  
Db 121 ITMFFMLALMASLYVHMFMLARLHKRIAVLPCTGTIRQANMKMGATITLILIGVFWVC 180  
QY 258 WAPFFLHLFIYISCPNYPVCVCFMSHFNLYLILIM 292  
Db 181 WAPFFLHLFIYISCPNYPVCVCFMSHFNLYLILIM 215  
RESULT 3  
JC2193  
melanocortin receptor, MC5 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 24-Sep-1999  
C:Accession: JC2193  
R:Griffon, N.; Mignon, V.; Facchinetti, P.; Diaz, J.; Schwartz, J.C.; Sokoloff, P.  
Biochem. Biophys. Res. Commun. 200, 1007-1014, 1994  
A:Title: Molecular cloning and characterization of the rat fifth melanocortin receptor.  
A:Reference number: JC2193; MUID:94234987; PMID:8179577  
A:Accession: JC2193  
A:Molecule type: DNA  
A:Residues: 1-325 <GRI>  
A:Cross-references: GB:L27081; NID:9435606; PIDN:AAAA1577.1; PID:9435607  
C:Superfamily: melanocortin receptor  
C:Keywords: G protein-coupled receptor; receptor; transmembrane protein  
F:37-63/Domain: transmembrane #status predicted <TM1>  
F:117-138/Domain: transmembrane #status predicted <TM3>  
F:159-179/Domain: transmembrane #status predicted <TM4>  
F:193-211/Domain: transmembrane #status predicted <TM5>  
F:240-263/Domain: transmembrane #status predicted <TM6>  
F:276-297/Domain: transmembrane #status predicted <TM7>

Query Match 60.3%; Score 1041; DB 2; Length 325;  
Best Local Similarity 65.0%; Pred. No. 8.1e-78;  
Matches 202; Conservative 45; Mismatches 60; Indels 4; Gaps 3;

QY 26 NATES--LGKGYPD-GCYBQLFVSPVFTLVGLVILLENILVIAIAKNNLHSPMYFF 82  
Db 15 NASEDNILGQNVNKNKSCACEDMGIAVEVFTLVGLVILLENILVIAIAKNNLHSPMYFF 74  
QY 83 ICSLAVADMLVSVNGSETIVITLLNSTD-TDAQSFVNIDNVIDSVICSSLLASCSLL 141  
Db 75 VGS LAVADMLVSVNSNAWETITTYLINNHKVVIADTFVRHIDNVFDSMICSISVASMCSLL 134  
QY 142 STAVDRYFTIFAYALQYHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICLTMF 201  
Db 135 ATAVDRYFTIFAYALQYHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICLTMF 194  
QY 202 FTMLALMASLYVHMFMLARLHKRIAVLPCTGTIRQANMKMGATITLILIGVFWVCWAPF 261  
Db 195 FTMLFVWSLYIHMFLLARNHVKRIASPRYSNVRQASMKGATITLMLGIIIVCWSPF 254  
QY 262 FTHLFIYISCPNYPVCVCFMSHFNLYLILMCSNIDPLIYALRSQELRKTKEIKICCPY 321  
Db 255 FLHLILMISCPNYPVCVCFMSHFNLYLILMCSNIDPLIYALRSQELRKTKEIKICCHG 314  
QY 322 LGGCLDLSSRY 332  
Db 315 FRRTCTLLGRY 325

RESULT 4  
I49008  
melanocortin-5 receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Sep-1999  
C:Accession: I49008; A54245; JC2244  
R:Pathi, Z.; Iben, L.G.; Parker, E.M.  
Neurochem. Res. 20, 107-113, 1995  
A:Title: Cloning, expression, and tissue distribution of a fifth melanocortin receptor  
A:Reference number: I49008; MUID:95258173; PMID:7739752  
A:Accession: I49008  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-372 <RES>  
A:Cross-references: EMBL:U08354; NID:9522165; PIDN:AAA76585.1; PID:9522166  
R:Labbe, O.; Desarnaud, F.; Eggerickx, D.; Vassart, G.; Parmentier, M.  
Biochemistry 33, 4543-4549, 1994  
A:Title: Molecular cloning of a mouse melanocortin 5 receptor gene widely expressed in the brain  
A:Reference number: A54245; MUID:94213827; PMID:8161509  
A:Accession: A54245  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 48-120, F', 122-372 <LAB>  
A:Cross-references: GB:X76295; NID:9498973; PIDN:CAA53943.1; PID:9498974  
A:Experimental source: clone HGMP01B  
A:Note: sequence extracted from NCBI backbone (NCBIP:145988)  
R:Gantz, I.; Shimoto, Y.; Konda, Y.; Miwa, H.; Dickinson, C.J.; Yamada, T.  
Biochem. Biophys. Res. Commun. 200, 1214-1220, 1994  
A:Title: Molecular cloning, expression, and characterization of a fifth melanocortin receptor  
A:Reference number: JC2244; MUID:94241974; PMID:8185570  
A:Accession: JC2244  
A:Molecule type: DNA  
A:Residues: 48-372 <GAN>  
A:Cross-references: GB:L22527; NID:9468377; PIDN:AAA21337.1; PID:9468378  
C:Comment: This protein responds to melanocortins with an increase in intracellular cAMP  
C:Superfamily: melanocortin receptor  
C:Keywords: receptor; transmembrane protein  
F:84-109/Domain: transmembrane #status predicted <TM1>  
F:121-144/Domain: transmembrane #status predicted <TM2>  
F:164-185/Domain: transmembrane #status predicted <TM3>  
F:206-226/Domain: transmembrane #status predicted <TM4>  
F:232-257/Domain: transmembrane #status predicted <TM5>  
F:287-310/Domain: transmembrane #status predicted <TM6>  
F:324-344/Domain: transmembrane #status predicted <TM7>

Query Match 59.3%; Score 1023.5; DB 2; Length 372;  
Best Local Similarity 66.4%; Pred. No. 2.5e-76;  
Matches 194; Conservative 44; Mismatches 53; Indels 1; Gaps 1;

```
Qy 42 EQLFVSPVFTLVGLVISLLENILVIVAIAKNNLHSPMYFFICSLAVADMVLSVNSGET 101
Db 81 EEMGIAVEFTLVGLVSLLENILVIGAVKNNLHSPMYFVVGSLAVADMVLSVNSAWET 140
Qy 102 IVITLLNSTD-TDAQSFVNIDNVDVSCSSLLASCSLSIAVDRTFTFYALQYHNI 160
Db 141 VTYILLNKKHLVIAIDTFRHHIDNVDSMICSIVVSMCSLLAIAVDRTFTFYALRYHHI 200
Qy 161 MTRRVGIIISCIWAACVSGILFIYSDSTAVIICLTMTFMTLALMASLYVHMFILMAR 220
Db 201 MTRRSVGIACIWTFCISGIVFIYIESKYVICLISMEFTMLFVMSLYIIMFLLAR 260
Qy 221 LHKRIAVLPOTGTIRGCANMKGAITLILGVFVWCWAPFHLHIFVISCQPNQYCVCF 280
Db 261 NHVKRIAASPRYNSVRQTSKMGAITLMLGLGIVCWSPPFLHLILMISCPQNVYCSCF 320
Qy 281 MSHENLYLILIMCNSIIDPLIYALRSOELKRTFKEICCYPLGGLDLSRRY 332
Db 321 MSYFNMYLILIMCNSVIDPLIYALRSOEMRRTFKEIVCCHGFRPRCLLGGY 372

RESULT 5
JC5592
melanocortin 5 receptor - human
C:Species: Homo sapiens (man)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 07-May-1999
C:Accession: JC5592
R:Fraendberg, P.A.; Xu, X.; Chhajlani, V.
Biochem. Biophys. Res. Commun. 236, 489-492, 1997
A:Title: Glutamine-235 and arginine-272 in human melanocortin 5 receptor determines its
A:Reference number: JC5592; MUID:97382462; PMID:9240466
A:Accession: JC5592
A:Molecule type: protein
A:Residues: 1-325 <FR2>
C:Comment: This protein is the melanocortin receptor with low affinity towards alpha-MSH
C:Superfamily: melanocortin receptor
F:77-100/Domain: transmembrane #status predicted <TM1>
F:115-138/Domain: transmembrane #status predicted <TM2>
F:156-179/Domain: transmembrane #status predicted <TM3>
F:187-210/Domain: transmembrane #status predicted <TM4>
F:240-263/Domain: transmembrane #status predicted <TM5>
F:274-297/Domain: transmembrane #status predicted <TM6>

Query Match 59.2%; Score 1022.5; DB 2; Length 325;
Best Local Similarity 62.0%; Pred. No. 2.7e-76;
Matches 207; Conservative 42; Mismatches 72; Indels 13; Gaps 5;
Qy 1 MNSTLQHGHTSLHFWRNSTYGOHGNAT--ESLKGYPDGGCYQLFVSPVFTLVGLVIS 58
Db 1 MNSSFH-----LHFLDLNLNATGNSLGNPNVKNKSSP--C-EDMGIAVEFTLVGLVIS 50
Qy 59 LLENILVIVAIAKNNLHSPMYFFICSLAVADMVLSVNSGETIVITLLNSTD-TDAQSF 117
Db 51 LLENILVIGAVKNNLHSPMYFFVCSLAVADMVLSVNSAWETITVLLNKKHLVIADAF 110
Qy 118 TVNIDNVDSVICSLLASCSLSIAVDRTFTFYALQYHNIIMTVRRVGIISCIWAAC 177
Db 111 VRHIDNVDSMICISVWASCSLLAIAVDRTFTFYALRYHHIMTARRSGAIIAGIWAFC 170
Qy 178 TVSGILFIYSDSTAVIICLTMTFMTLALMASLYVHMFILMARHRIKRIAVLPGTGTIRQ 237
Db 171 TGCIGVFIYSESYVILCLISMEFFAMFLVLSLYIIMFLLARTHVRIALCPGASARQ 230
Qy 238 GANKMGAITLILGVFVWCWAPFHLHIFVISCQPNQYCVCFMSHFNLYLILIMCNSII 297
Db 231 RTSMQGAQVTVTMLLGVFTVCWAPFHLHIFVISCQPNQYCVCFMSHFNLYLILIMCNSVM 290
Qy 298 DPLIYALRSOELKRTFKEICCYPLGGLDLSRR 331
Db 291 DPLIYALRSOEMRKTFFKEIICCRGFRIACSPFRR 324

Query Match 59.2%; Score 1022.5; DB 2; Length 325;
Best Local Similarity 62.0%; Pred. No. 2.7e-76;
Matches 207; Conservative 42; Mismatches 72; Indels 13; Gaps 5;
Qy 1 MNSTLQHGHTSLHFWRNSTYGOHGNAT--ESLKGYPDGGCYQLFVSPVFTLVGLVIS 58
Db 1 MNSSFH-----LHFLDLNLNATGNSLGNPNVKNKSSP--C-EDMGIAVEFTLVGLVIS 50
Qy 59 LLENILVIVAIAKNNLHSPMYFFICSLAVADMVLSVNSGETIVITLLNSTD-TDAQSF 117
Db 51 LLENILVIGAVKNNLHSPMYFFVCSLAVADMVLSVNSAWETITVLLNKKHLVIADAF 110
Qy 118 TVNIDNVDSVICSLLASCSLSIAVDRTFTFYALQYHNIIMTVRRVGIISCIWAAC 177
Db 111 VRHIDNVDSMICISVWASCSLLAIAVDRTFTFYALRYHHIMTARRSGAIIAGIWAFC 170
Qy 178 TVSGILFIYSDSTAVIICLTMTFMTLALMASLYVHMFILMARHRIKRIAVLPGTGTIRQ 237
Db 171 TGCIGVFIYSESYVILCLISMEFFAMFLVLSLYIIMFLLARTHVRIALCPGASARQ 230
Qy 238 GANKMGAITLILGVFVWCWAPFHLHIFVISCQPNQYCVCFMSHFNLYLILIMCNSII 297
Db 231 RTSMQGAQVTVTMLLGVFTVCWAPFHLHIFVISCQPNQYCVCFMSHFNLYLILIMCNSVM 290
Qy 298 DPLIYALRSOELKRTFKEICCYPLGGLDLSRR 331
Db 291 DPLIYALRSOEMRKTFFKEIICCRGFRIACSPFRR 324
```

```
RESULT 6
JN0764
melanocortin receptor 2 - human
C:Species: Homo sapiens (man)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 17-Mar-1999
C:Accession: JN0764; S37042; S40681
R:Chhajlani, V.; Muceniece, R.; Wikberg, J.E.S.
Biochem. Biophys. Res. Commun. 195, 866-873, 1993
A:Title: Molecular cloning of a novel human melanocortin receptor.
A:Reference number: S40681; MUID:93384614; PMID:8396929
A:Accession: JN0764
A:Molecule type: DNA
A:Residues: 1-325 <CHH>
A:Cross-references: EMBL:Z25470
A:Experimental source: brain
C:Superfamily: melanocortin receptor
C:Keywords: glycoprotein; receptor; transmembrane protein
F:38-61/Domain: transmembrane #status predicted <TM1>
F:74-97/Domain: transmembrane #status predicted <TM2>
F:115-138/Domain: transmembrane #status predicted <TM3>
F:156-179/Domain: transmembrane #status predicted <TM4>
F:187-211/Domain: transmembrane #status predicted <TM5>
F:240-265/Domain: transmembrane #status predicted <TM6>
F:274-297/Domain: transmembrane #status predicted <TM7>
F:2,20,28/Binding site: carbohydrate (Asn) #status predicted

Query Match 58.1%; Score 1003.5; DB 2; Length 325;
Best Local Similarity 61.1%; Pred. No. 9.5e-75;
Matches 204; Conservative 43; Mismatches 74; Indels 13; Gaps 5;
Qy 1 MNSTLQHGHTSLHFWRNSTYGOHGNAT--ESLKGYPDGGCYQLFVSPVFTLVGLVIS 58
Db 1 MNSSFH-----LHFLDLNLNATGNSLGNPNVKNKSSP--C-EDMGIAVEFTLVGLVIS 50
Qy 59 LLENILVIVAIAKNNLHSPMYFFICSLAVADMVLSVNSGETIVITLLNSTD-TDAQSF 117
Db 51 LLENILVIGAVKNNLHSPMYFFVCSLAVADMVLSVNSAWETITVLLNKKHLVIADAF 110
Qy 118 TVNIDNVDSVICSLLASCSLSIAVDRTFTFYALQYHNIIMTVRRVGIISCIWAAC 177
Db 111 VRHIDNVDSMICISVWASCSLLAIAVDRTFTFYALRYHHIMTARRSGAIIAGIWAFC 170
Qy 178 TVSGILFIYSDSTAVIICLTMTFMTLALMASLYVHMFILMARHRIKRIAVLPGTGTIRQ 237
Db 171 TGCIGVFIYSESYVILCLISMEFFAMFLVLSLYIIMFLLARTHVRIALCPGASARQ 230
Qy 238 GANKMGAITLILGVFVWCWAPFHLHIFVISCQPNQYCVCFMSHFNLYLILIMCNSII 297
Db 231 GPANQGAQVTVTMLLGVFTVCWAPFHLHIFVISCQPNQYCVCFMSHFNLYLILIMCNSVM 290
Qy 298 DPLIYALRSOELKRTFKEICCYPLGGLDLSRR 331
Db 291 DPLIYALRSOEMRKTFFKEIICCRGFRIACSPFRR 324

RESULT 7
S43850
melanocortin 3 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 24-Sep-1999
C:Accession: S43850; S37153
R:Desarnaud, F.; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.
Biochem. J. 299, 367-373, 1994
A:Title: Molecular cloning, functional expression and pharmacological characterization
A:Reference number: S43850; MUID:94226597; PMID:8172596
A:Accession: S43850
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <DES>
A:Cross-references: EMBL:X74983; NID:9400473; PIDN:CAA52918.1; PID:9400474
C:Superfamily: melanocortin receptor
```

Query Match 57.6%; Score 994; DB 2; Length 323;  
Best Local Similarity 61.7%; Pred. No. 5.7e-74;  
Matches 182; Conservative 53; Mismatches 52; Indels 8; Gaps 4;

QY 27 ATESLGKGYDGGCYEQOLFVSPFVTLGVISLENILVIVATAKKNLHSPMYFFICSL 86  
DQ 26 ASNRSGSGF---C-EQVFIKPEVFLALGVLSLENILVILAVRNGNLHSPMYFFICSL 80  
QY 87 AVADMLVSVNGSETVITLLNSTD-TDAQSFVTVNIDVSVICSSLLASICSLSIAV 145  
DQ 81 AADMLVSVLSNSETMTIAVINSDSLTLEQDFQHMNDIFDSMICSLSVASICNLALAI 140  
QY 146 DRYFTIFALQYHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVIICLITMFFTML 205  
DQ 141 DRYFTIFALRYHSIMTVRKALTLIGVIWCCGIGVWFYIYSESKWIVCLITMFFAMV 200  
QY 206 ALMASLYVHFLMARLHRIKRIAVLPDGTGTI--ROGANMKGATLTILIGVVFVWCPAPFL 263  
DQ 201 LLMGTLYIHMFLFARLHVORIAVLPAGVVPQOQSCMKGAVTITLLGVFIKWPAPFL 260  
QY 264 HLIFVISCQPNYCVCFMSHFNLYLILMCSNIIDPLIYALRSOELRKTFKEILC 318  
DQ 261 HLVLITCPNPICICYTAHFNTYLVLMCSNIDPLIYAFRSLELRNTFKEILC 315

RESULT 8  
B46647  
melanocortin receptor 3.- human  
C:Species: Homo sapiens (man)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998  
R:Gantz, I.; Konda, Y.; Tashiro, T.; Shimoto, Y.; Miwa, H.; Munzert, G.; Watson, S.J.; J. Biol. Chem. 268, 8246-8250, 1993  
A:Title: Molecular cloning of a novel melanocortin receptor.  
A:Reference number: A46647; MUID:93216807; PMID:8463333  
A:Accession: B46647  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-360 <GAN>  
A:Note: sequence extracted from NCBI backbone (NCBIP:129161)  
C:Genetics:  
A:Gene: GDB:MC3R  
A:Cross-references: GDB:138780  
A:Map position: 20q13.2-20q13.3  
C:Superfamily: melanocortin receptor

Query Match 57.2%; Score 987.5; DB 2; Length 360;  
Best Local Similarity 64.3%; Pred. No. 2.1e-73;  
Matches 180; Conservative 49; Mismatches 48; Indels 3; Gaps 2;

QY 42 EQLFVSPFVTLGVISLENILVIVATAKKNLHSPMYFFICSLAVADMLVSVNGSET 101  
DQ 73 EQVFIKPEIFLSIGVLSLENILVILAVRNGNLHSPMYFFICSLAVADMLVSVNALET 132  
QY 102 IVITLLNSTD-TDAQSFVTVNIDVSVICSSLLASICSLSIAVDRYFTIFALQYHNI 160  
DQ 133 IMIAVHSDDYTFEDQFIQHMNDIFDSMICSLSIASICNLALAVDRYFTIFALRYHSI 192  
QY 161 MTVRRVGIISCIWAACVSGILFIYSDSTAVIICLITMFFTMLMASLYVHFLMAR 220  
DQ 193 MTVRKALTLIAVWCCGCVGVVFIYSESKWIVCLITMFFAMLLMGTLYVHMFLEAR 252  
QY 221 LHKRIAVLPDGTGTI--ROGANMKGATLTILIGVVFVWCPAPFLHLIFVISCQPNYCV 278  
DQ 253 LHVKRIALPPADGAVAPQOQSCMKGAVTITLLGVFIKWPAPFLHLVLIITCPNPTCT 312  
QY 279 CFMSHFNLYLILMCSNIIDPLIYALRSOELRKTFKEILC 318  
DQ 313 CYTAHFNTYLVLMCSNIDPLIYAFRSLELRNTFKEILC 352

RESULT 9  
S36636

melanocortin receptor 3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 02-Jun-2000  
C:Accession: A48254; S36636  
R:Roselli-Rehuss, L.; Mountjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatiro  
Proc. Natl. Acad. Sci. U.S.A. 90, 8856-8860, 1993  
A:Title: Identification of a receptor for gamma melanotropin and other proopiomelanoc  
A:Reference number: A48254; MUID:94022273; PMID:8415620  
A:Accession: A48254  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-323 <ROS>  
A:Cross-references: EMBL:X70667; NID:g396551; PIDN:CAA50005.1; PID:g396552  
A:Note: submitted to the EMBL Data Library, January 1993  
A:Note: in Genbank entry RMC3RA, release 113.0, the source is designated as Rattus r  
C:Genetics:  
A:Gene: MC3-R  
C:Superfamily: melanocortin receptor  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 55.9%; Score 965; DB 2; Length 323;  
Best Local Similarity 59.0%; Pred. No. 1.3e-71;  
Matches 180; Conservative 55; Mismatches 62; Indels 8; Gaps 4;

QY 17 NRSTYQGHGNATESLGKGYDGGCYEQOLFVSPFVTLGVISLENILVIVATAKKNLH 76  
DQ 16 NLSQHPAAPSASNRSGF---C-EQVFIKPEVFLALGVLSLENILVILAVRNGNLH 70  
QY 77 SPMYFFICSLAVADMLVSVNGSETVITLLNSTD-TDAQSFVTVNIDVSVICSSLLA 135  
DQ 71 SPMYFFICSLQADMLVSVLSNSETMTIAVINSDSLTLEQDFQHMNDIFDSMICSLSIA 130  
QY 136 SICSLSIAVDRYFTIFALQYHNIMTVRRVGIISCIWAACVSGILFIYSDSTAVII 195  
DQ 131 SICNLLAIAVDRYFTIFALRYHSIMTVRKALSLIAVWCCGIGVWFYIYSESKWIV 190  
QY 196 CLITMFFTMLMASLYVHFLMARLHRIKRIAVLPDGTGTI--ROGANMKGATLTILIGV 253  
DQ 191 CLITMFFAMVLLMGTLYIHMFLFARLHVORIAVLPADGAVAPQOQSCMKGAVTITLLGV 250  
QY 254 FVVCWAPFLHLIFVISCQPNYCVCFMSHFNLYLILMCSNIIDPLIYALRSOELRKTF 313  
DQ 251 FIFCWAPFLHLVLIITCPNPTCYICTAHFNTYLVLMCSNIDPLIYAFRSLELRNTF 310  
QY 314 KEIIC 318  
DQ 311 KEILC 315

RESULT 10  
I46416  
melanocyte-stimulating hormone receptor - sheep  
C:Species: Ovis orientalis aries, Ovis amon aries (domestic sheep)  
C:Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 24-Sep-1999  
C:Accession: I46416; S43120  
R:Barrett, P.; MacDonald, A.; Helliwell, R.; Davidson, G.; Morgan, P.  
J. Mol. Endocrinol. 12, 203-213, 1994  
A:Title: Cloning and expression of a new member of the melanocyte-stimulating hormone  
A:Reference number: I46416; MUID:94338523; PMID:8060485  
A:Accession: I46416  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-325 <BAR>  
A:Cross-references: EMBL:X31369; NID:g467692; PIDN:CAA83239.1; PID:g467693  
A:Note: submitted to the EMBL Data Library, March 1994  
C:Superfamily: melanocortin receptor

Query Match 55.8%; Score 962.5; DB 2; Length 325;  
Best Local Similarity 59.2%; Pred. No. 2.2e-71;  
Matches 197; Conservative 41; Mismatches 86; Indels 9; Gaps 4;

QY 1 MNSTLQHGHTSLHFWNRSTYQGHGNATESLGKGYDGGCYEQOLFVSPFVTLGVISLL 60  
DQ 1 MNSTLQHGHTSLHFWNRSTYQGHGNATESLGKGYDGGCYEQOLFVSPFVTLGVISLL 60





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:04:01 ; Search time 14 Seconds  
(without alignments)  
983.581 Million cell updates/sec

Title: US-09-884-211a-4

Perfect score: 1726

Sequence: 1 MNSTLQGHMHTSLHFWNRST.....FKEIICCYPLGLGLDLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	1664	96.4	332	1	MC4R_PIG	O97504 sus scrofa
2	1638.5	94.9	332	1	MC4R_HUMAN	P32245 homo sapien
3	1628	94.3	332	1	MC4R_RAT	P70596 rattus norv
4	1590	92.1	332	1	MC4R_BOVIN	Q9qlj8 bos taurus
5	1041	60.3	325	1	MC5R_RAT	P35345 rattus norv
6	1029.5	59.6	325	1	MC5R_PANTR	Q9tt23 pan troglod
7	1026.5	59.5	325	1	MC5R_MOUSE	P41149 mus musculu
8	1025.5	59.4	325	1	MC5R_HUMAN	P33032 homo sapien
9	994	57.6	323	1	MC3R_MOUSE	P33033 mus musculu
10	982.5	56.9	360	1	MC3R_HUMAN	P41968 homo sapien
11	967.5	56.1	325	1	MC5R_BOVIN	P56451 bos taurus
12	965	55.9	323	1	MC3R_RAT	P32244 rattus norv
13	962.5	55.8	325	1	MC5R_SHEEP	P41983 ovis aries
14	941	54.5	294	1	MC5R_PIG	Q9mzv8 sus scrofa
15	928	53.8	184	1	MC4R_MOUSE	P56450 mus musculu
16	817.5	47.4	314	1	MSHR_CHICK	P55167 gallus gall
17	781.5	45.3	317	1	MSHR_CAPCA	P56443 capreolus c
18	781.5	45.3	317	1	MSHR_DAMDA	P56446 dama dama (
19	777.5	45.0	317	1	MSHR_ALCNA	P56442 alces alces
20	774.5	44.9	317	1	MSHR_BOVIN	P47798 bos taurus
21	770	44.6	317	1	MSHR_RANTA	P56448 rangifer ta
22	769.5	44.6	317	1	MSHR_CAPHI	P56444 capra hircu
23	769.5	44.6	317	1	MSHR_CEREL	P56445 cervus elap
24	769.5	44.6	317	1	MSHR_SHEEP	O19037 ovis aries
25	768	44.5	317	1	MSHR_OVIMO	P56447 ovibos mosc
26	766.5	44.4	283	1	MSHR_PIG	Q9tu05 sus scrofa
27	766	44.4	317	1	MSHR_CANFA	O77616 canis famil
28	766	44.4	317	1	MSHR_VULVU	Q29154 vulpes vulp
29	755.5	43.8	317	1	MSHR_PANTR	Q9tuk4 pan troglod
30	754.5	43.7	317	1	MSHR_HUMAN	Q01726 homo sapien
31	752.5	43.6	315	1	MSHR_MOUSE	Q01727 mus musculu
32	741.5	43.0	292	1	MSHR_HORSE	P79166 equus cabal
33	723	41.9	297	1	ACTR_HUMAN	Q01718 homo sapien

## ALIGNMENTS

### RESULT 1

ID	MC4R_PIG	STANDARD;	PRT;	332 AA.
AC	O97504; Q9N274; Q9N141;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Melanocortin-4 receptor (MC4-R).			
GN	MC4R.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=LMD; TISSUE=Kidney;			
RA	Ito Y., Minezawa M.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 73-320 FROM N.A., AND VARIANT ASN-298.			
RX	MEDLINE=20122164; PubMed=10656927;			
RA	Kim K.S., Larsen N., Short T., Plastow G., Rothschild M.F.;			
RT	"A missense variant of the porcine melanocortin-4 receptor (MC4R) gene is associated with fatness, growth, and feed intake traits.";			
RL	Mamm. Genome 11:131-135(2000).			
RP	[3]			
RC	SEQUENCE OF 75-142 FROM N.A.			
RA	Matteri R.L., Dyer C.J.;			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
CC	ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.			
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE CYCLASE (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AB021664; BAA36170.1; -			
DR	EMBL; AF087937; AAF31753.1; -			
DR	EMBL; AF227727; AAF34778.1; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; P000237; GPCRHHODPSN.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Phosphorylation; Lipoprotein; Palmitate; Polymorphism.			
FT	DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).			

Q9tu77 ovis aries  
Q64326 mus musculus  
P34974 bos taurus  
P70115 mesocricetu  
Q921s9 cavia porce  
Q92633 homo sapien  
Q61130 mus musculus  
P46628 ovis aries  
Q28031 bos taurus  
P47731 homo sapien  
P30951 rattus norv  
P35412 mus musculus

34 721 41.8 295 1 ACTR\_SHEEP  
35 721 41.8 296 1 ACTR\_MOUSE  
36 720 41.7 297 1 ACTR\_BOVIN  
37 720 41.7 297 1 ACTR\_MESAU  
38 688 39.9 297 1 ACTR\_CAVPO  
39 358.5 20.8 364 1 EDG2\_HUMAN  
40 356 20.6 364 1 EDG2\_MOUSE  
41 348 20.2 393 1 EDG2\_SHEEP  
42 347 20.1 364 1 EDG2\_BOVIN  
43 346 20.0 334 1 GP12\_HUMAN  
44 337 19.5 334 1 GP12\_RAT  
45 335 19.4 334 1 GP12\_MOUSE







DE Melanocortin-4 receptor (MC4-R).  
GN MC4R.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND VARIANTS ALA-145 AND THR-172.  
RC STRAIN=Holstein;  
RX MEDLINE=21422894; PubMed=11531696;  
RA Haegeman A., Coopman F., Jacobs K., Mattheeuws M., Van Zeven A.,  
RA Peelman L.J.;  
RT "Bovine melanocortin receptor 4: cDNA sequence, polymorphisms and  
RT mapping";  
RL AnIm. Genet. 32:189-192(2001).  
CC -1- FUNCTION: RECEPTOR SPECIFIC TO THE HEPTAPEPTIDE CORE COMMON TO  
CC ADRENOCORTICOTROPIC HORMONE AND ALPHA-, BETA-, AND GAMMA-MSH.  
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE  
CC CYCLASE (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL: AF265221; AAC17639.1; -  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC Pfam: PF00001; 7tm\_1; 1.  
CC PRINTS: PR00237; GPCRRHODOPS.  
CC PROSITE: PS00237; G-PROTEIN-RECEP\_FL1; 1.  
CC PROSITE: PS00262; G-PROTEIN-RECEP\_FL2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
CC Phosphorylation; Lipoprotein; Palmitate; Polymorphism.  
CC DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 44 69  
CC DOMAIN 70 81  
CC TRANSMEM 82 106  
CC DOMAIN 107 123  
CC TRANSMEM 124 145  
CC DOMAIN 146 165  
CC TRANSMEM 166 186  
CC DOMAIN 187 191  
CC TRANSMEM 192 215  
CC DOMAIN 216 248  
CC TRANSMEM 249 271  
CC DOMAIN 272 280  
CC TRANSMEM 281 304  
CC DOMAIN 305 332  
CC CARBOHYD 2 2  
CC CARBOHYD 17 17  
CC CARBOHYD 26 26  
CC CARBOHYD 318 318  
CC LIPID 145 145  
CC VARIANT 172 172  
CC SEQUENCE 332 AA; 36620 MW; C28356955F9D8FBD CRC64;  
CC  
CC Query Match 92.1%; Score 1590; DB 1; Length 332;  
CC Best Local Similarity 93.1%; Pred. No. 5.8e-100;  
CC Matches 309; Conservative 8; Mismatches 15; Indels 0; Gaps 0;  
CC  
CC 1 MNSTLQGHMHTSLHFWNRSTYGOHGNATESLKGYPDGGCYEQLFVSPFVTLGVISLL 60  
CC ||||| ||||| ||||| : | : ||||| ||||| ||||| ||||| ||||| ||||| |||||  
CC 1 MNSTQPLGHMHTSLHWSNRSAHGMPNTVNSLARGSDGCGYEQLFVSPFVTLGVISLL 60  
CC  
CC 61 ENILVIVATAKNKLHSPMYFFICSILAVADMVLSVNSGSETIVITLLNSTDTDAQSFTYN 120  
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
CC 61 ENILVIVATAKNKLHSPMYFFICSILAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVD 120

QY 121 IDNVIDSVICSSLLASICSLLSIADVRYFTTFYALQVYHNMVTRVGVIIISCIWAACVTS 180  
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 121 IDNVIDSVICSSLLASICSLLSIADVRYFTTFYALQVYHNMVTRVGVIIISCIWAACVTS 180  
QY 181 GILFIYSDSTAVIICLITMEFTMALMASLYVHMFMLMARLHRIKRIAVLPOTGTIRQGAN 240  
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 181 GVLFIIYSDSSAVIICLITVEFTMALMASLYVHMFMLMARLHRIKRIAVLPOTGTIRQGAN 240  
QY 241 MKGATITLILGVFVWCWAPFELHLIFVISPQNPYCVCFMSHNFYLILIMCNSIIDPL 300  
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 241 MKGATITLILGVFVWCWAPFELHLIFVISPQNPYCVCFMSHNFYLILIMCNSIIDPL 300  
QY 301 IYALRSQELRKTFKEIICCYPLGGLCLDLSRRY 332  
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 301 IYALRSQELRKTFKEIICCYPLGGLCLDLSRRY 332  
  
RESULT 5  
MC5R\_RAT ID MC5R\_RAT STANDARD; PRT; 325 AA.  
AC P35345;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Melanocortin-5 receptor (MC5-R).  
GN MC5R.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Striatum;  
RX MEDLINE=94234987; PubMed=8179577;  
RA Griffon N., Mignon V., Facchinetti P., Diaz J., Schwartz J.C.,  
RA Sokoloff P.;  
RT "Molecular cloning and characterization of the rat fifth melanocortin  
RT receptor";  
RL Biochem. Biophys. Res. Commun. 200:1007-1014(1994).  
CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE  
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE  
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: VERY LOW EXPRESSION LEVELS IS DETECTED IN  
CC BRAIN, WHILE HIGH LEVELS ARE FOUND IN ADRENALS, STOMACH, LUNG AND  
CC SPLEEN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL: L27081; AAA41577.1; -  
CC PIR: JC2193; JC2193.1; -  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC Pfam: PF00001; 7tm\_1; 1.  
CC PROSITE: PS00237; G-PROTEIN-RECEP\_FL1; 1.  
CC PROSITE: PS00262; G-PROTEIN-RECEP\_FL2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
CC Phosphorylation; Lipoprotein; Palmitate.  
CC DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 38 61  
CC DOMAIN 62 73  
CC TRANSMEM 74 97  
CC DOMAIN 98 114  
CC TRANSMEM 115 138  
CC DOMAIN 139 155  
CC CYTOPLASMIC (POTENTIAL).





RA Hattat N., Dixon C., Ray A.J., Phillips S.R., Cunliffe W.J., Dale M.,  
 RT Todd C., Meggit S., Birch-Machin M.A., Rees J.L.;  
 RT "Expression, candidate gene, and population studies of the  
 RL melanocortin 5 receptor.";  
 RL J. Invest. Dermatol. 116:564-570(2001).  
 CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE  
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE  
 CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: IS EXPRESSED IN THE BRAIN BUT NOT IN THE  
 CC MELANOMA CELLS.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 DR EMBL; Z25470; CAA80962.1; -;  
 DR EMBL; L27080; AAB59566.1; -;  
 DR EMBL; U08353; AAB60376.1; -;  
 DR Genbank; HGNC:6933; MC5R.  
 DR MIM; 600042; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate; Polymorphism.  
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 38 61 1 (POTENTIAL).  
 FT DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 74 97 2 (POTENTIAL).  
 FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 115 138 3 (POTENTIAL).  
 FT DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 156 179 4 (POTENTIAL).  
 FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 187 211 5 (POTENTIAL).  
 FT DOMAIN 212 239 6 (POTENTIAL).  
 FT TRANSMEM 240 265 7 (POTENTIAL).  
 FT DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 274 297 7 (POTENTIAL).  
 FT DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 311 311 PALMITATE (POTENTIAL).  
 FT LIPID 312 312 PALMITATE (POTENTIAL).  
 FT VARIANT 209 209 F -> L.  
 FT CONFLICT 149 149 R -> A (IN REF. 2).  
 FT CONFLICT 221 234 ALPGASARQRTSM -> LCPGPALRGKPAW (IN  
 FT REF. 1).  
 FT CONFLICT 297 297 F -> Y (IN REF. 2).  
 SQ SEQUENCE 325 AA; 36600 MW; 8BEC17E1BDA059B8 CRC64;  
 Query Match 59.4%; Score 1025.5; DB 1; Length 325;  
 Best Local Similarity 62.0%; Pred. No. 3.6e-62;  
 Matches 207; Conservative 43; Mismatches 71; Indels 13; Gaps 5;  
 Qy 1 MNSTLQHGHTSLHFWNRSTYQGHGNAT--ESLKGYPDGGYQQLVSPFVTLGVIS 58  
 Db 1 MNSSFFH-----LHFLDLNLNATEGLSGPNVKNKSSP---C-EDMGIAVEVTLGVIS 50  
 Qy 59 LLENILVIVAIAKNNLHSPMYFFICSLAVADMVLVSVNGSETIVTLNSTD--TDAQSF 117  
 Db 51 LLENILVIGAIVKNNLHSPMYFFVFCVSLAVADMVLVSVSSAWETITIVLLNKNHVLVADAF 110

Qy 118 TVNIDNVDSVICSLLASIGLSIAVDRTTFYALQYHNIMTVRRVGIISCIWAAC 177  
 Db 111 VRHIDNVFDSMICISVWASMCSSLAIAVDRTTFYALRYHIMTARSGGALIAGIWAFC 170  
 Qy 178 TVSGILFIYSDSTAVIICLTMTFTMALMASLYVHMFMLARLHIKRIAVLPDGTGTRQ 237  
 Db 171 TCGGVFTLYSESTYVILCLISMFAMFLVLSYIHMFLARTHVKKRAALPGASSARQ 230  
 Qy 238 GANKMGATLITLIGVFVWCPAFELHLIFVISCPONPYCVCFMSHFNLYLILIMCNSII 297  
 Db 231 RTSQGVATVTLGLVFTVWAPFELHLTLMLSCPQNLCSRFMSHFNLYLILIMCNSVM 290  
 Qy 298 DPLIYALRSQELRKTFKEIICYPGLGLCLDSRR 331  
 Db 291 DPLIYAFRSQEMRKTFKEIICRGFRACSFRR 324  
 RESULT 9  
 MC3R\_MOUSE STANDARD; PRT; 323 AA.  
 AC P33033;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Melanocortin-3 receptor (MC3-R).  
 GN MC3R.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=94226597; PubMed=8172596;  
 RX Desarnaud F., Labbe O., Eggerickx D., Vassart G., Parmentier M.;  
 RT "Molecular cloning, functional expression and pharmacological  
 RL characterization of a mouse melanocortin receptor gene.";  
 RL Biochem. J. 299:367-373(1994).  
 CC -!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THIS  
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE  
 CC CYCLASE.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: BRAIN.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 DR EMBL; X74983; CAA52918.1; -;  
 DR PIR; S37153; S37153.  
 DR MGD; MGI:96929; Mc3r.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 38 63 1 (POTENTIAL).  
 FT DOMAIN 64 75 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 76 100 2 (POTENTIAL).  
 FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 119 140 3 (POTENTIAL).  
 FT DOMAIN 141 160 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 161 181 4 (POTENTIAL).  
 FT DOMAIN 182 186 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 187 210 5 (POTENTIAL).  
 FT DOMAIN 211 245 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 246 268 6 (POTENTIAL).  
 FT DOMAIN 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 299 301 7 (POTENTIAL).  
 FT DOMAIN 302 323 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 315 PALMITATE (POTENTIAL).  
 SQ SEQUENCE 323 AA; 35806 MW; F4B7B02FAA87B7B CRC64;  
 Query Match 57.6%; Score 994; DB 1; Length 323;  
 Best Local Similarity 61.7%; Pred. No. 4.6e-60;  
 Matches 180; Conservative 53; Mismatches 52; Indels 8; Gaps 4;  
 QY 27 ATESLGKGYDGGCYQLFVSPFVFTLVGLVSLLENLIVIVAIAKKNLHSPMYFFICSL 86  
 DB 26 ASNRSGSF---C-EQVFKPEVFLALGIVSLMENLIVAVRGNLHSPMYFFICSL 80  
 QY 87 AVADMLVSVNGSETIVITLLNSTD-TDAQSFVNDVNDVSVCSLLASICSLSIAV 145  
 DB 81 AAADMLVSLNSLETIMIAVINSLSLTLEQDFQHMNDIPDSMICISLVASICNLLAIAI 140  
 QY 146 DRYFTFYALQYHINIMTVRGVGIISCIWAACVSGILEFTIYSDSTAVIICLTMTFMTL 205  
 DB 141 DRVTIFYAURHSIMTVRKALTLGVIWCCGICGVWFIYSESKWIVCLITMFFAMV 200  
 QY 206 ALMASLYVHMFMLARLHRIKRIAVLPGTGTI--RQGANMKGAITLTILGVFVVCWAPFFL 263  
 DB 201 LLMGTLVIHMFARLHVQRIAVLPAGVVPQOHSCKMGAVITILLGVFICWAPFFL 260  
 QY 264 HLIFYSCPNQVCFMSHFNLYLIMCNSIIDPLLYALRSQELRKTFKEIC 318  
 DB 261 HLVLITCTPNYCICYTAHFNTYLVLMCNSVIDPLIYAFRSLELRNFTKEIC 315  
 RESULT 10  
 MC3R\_HUMAN STANDARD; PRT; 360 AA.  
 AC P41968; Q9H517;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Melanocortin-3 receptor (MC3-R).  
 GN MC3R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93216807; PubMed=8463333;  
 RA Gantz I., Konda Y., Tashiro T., Shimoto Y., Miwa H., Munzert G.,  
 RA Watson S.J., Delvalle J., Yamada T.;  
 RT "Molecular cloning of a novel melanocortin receptor.";  
 RL J. Biol. Chem. 268:8246-8250(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Levenshalo M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THIS  
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE  
 CC CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: BRAIN, PLACENTAL, AND GUT TISSUES.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; L06155; AAC13541.1; -;  
 DR EMBL; AL139824; CAC15480.1; -;  
 DR Genew; HGNC:6931; MC3R.  
 DR MIM; 155540; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 74 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 75 100 1 (POTENTIAL).  
 FT DOMAIN 101 112 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 113 137 2 (POTENTIAL).  
 FT DOMAIN 138 155 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 156 177 3 (POTENTIAL).  
 FT DOMAIN 178 197 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 198 218 4 (POTENTIAL).  
 FT DOMAIN 219 223 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 224 247 5 (POTENTIAL).  
 FT DOMAIN 248 282 6 (POTENTIAL).  
 FT TRANSSEM 283 305 6 (POTENTIAL).  
 FT DOMAIN 306 314 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 315 338 7 (POTENTIAL).  
 FT DOMAIN 339 360 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 352 352 PALMITATE (POTENTIAL).  
 FT CONFLICT 6 6 T -> K (IN REF. 1).  
 FT CONFLICT 81 81 V -> I (IN REF. 1).  
 SQ SEQUENCE 360 AA; 40072 MW; 0D2C61195C164C51 CRC64;  
 Query Match 56.9%; Score 982.5; DB 1; Length 360;  
 Best Local Similarity 64.3%; Pred. No. 3e-59;  
 Matches 180; Conservative 49; Mismatches 48; Indels 3; Gaps 2;  
 QY 42 EQLFVSPFVFTLVGLVSLLENLIVIVAIAKKNLHSPMYFFICSLAVADMLVSVNGSET 101  
 DB 73 EQVFKPEVFLSGIVSLLENLIVAVRGNLHSPMYFFICSLAVADMLVSVNGSET 132  
 QY 102 IVITLLNSPD-TDAQSFVNDVNDVSVCSLLASICSLSIAVDRYFTFYALQYHNI 160  
 DB 133 IMIAVHSYLTFFEDQFQHMNDIPDSMICISLVASICNLLAIAVDRYFTFYALQYHNI 192  
 QY 161 MTRVRVGIISCIWAACVSGILEFTIYSDSTAVIICLTMTFMTLMAVHMFMLMAR 220



KW Phosphorylation; Lipoprotein; Palmitate.  
FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 38 63 1 (POTENTIAL).  
FT DOMAIN 64 75 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 76 100 2 (POTENTIAL).  
FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 119 140 3 (POTENTIAL).  
FT DOMAIN 141 160 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 161 181 4 (POTENTIAL).  
FT DOMAIN 182 186 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 187 210 5 (POTENTIAL).  
FT DOMAIN 211 245 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 246 268 6 (POTENTIAL).  
FT DOMAIN 269 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 278 301 7 (POTENTIAL).  
FT DOMAIN 302 323 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 2 32 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT LIPID 315 315 PALMITATE (POTENTIAL).  
SQ SEQUENCE 323 AA; 35866 MW; F4E4985C75E70A36 CRC64;

Query Match 55.9%; Score 965; DB 1; Length 323;  
Best Local Similarity 59.0%; Pred. No. 4e-58;  
Matches 180; Conservative 55; Mismatches 62; Indels 8; Gaps 4;

QY 17 NRSTYQGHGHNATESLGKGYPDGCGYQGFVSPVFTLVGLVISLLENILVIVATKKNLH 76  
Db 16 NLSQHPAASNRSGF---C-EQVFIKPEFVLGIVSLMENILVILAVRGNLH 70  
QY 77 SPMYFFCLSLQADMLVSLNSLETIMVIVNSDLSLEDOFQHDNDFSMICISLVA 130  
Db 71 SPMYFFCLSLQADMLVSLNSLETIMVIVNSDLSLEDOFQHDNDFSMICISLVA 130  
QY 136 SICSLSIADRVFTTFYALQYHINIMTVRRVGIISCIWAACVSGILFIYSDSTAVII 195  
Db 131 SICNLLAIADRVFTTFYALQYHINIMTVRRVGIISCIWAACVSGILFIYSDSTAVII 195  
QY 196 CLTTFMFTMLASLYVHMFARLHRIKRIALVPGTGTI--ROGANMKGATLTLLIGV 253  
Db 191 CLTTFMFTMLASLYVHMFARLHRIKRIALVPGTGTI--ROGANMKGATLTLLIGV 250  
QY 254 FVVCWAPFFLFIYFCISQPNVCYCFMSHFNLYLILMCNSIIDPLIYALRSQELRTKF 313  
Db 251 FVVCWAPFFLFIYFCISQPNVCYCFMSHFNLYLILMCNSIIDPLIYALRSQELRTKF 310  
QY 314 KEIIC 318  
Db 311 KEIIC 315

## RESULT 13

MC5R\_SHEEP  
ID MC5R\_SHEEP STANDARD; PRT; 325 AA.  
AC P41983;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Melanocortin-5 receptor (MC5-R).  
GN MC5R.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
SEQUENCE FROM N.A.  
RC TISSUE=Anterior pituitary;  
RX MEDLINE=94338523; PubMed=8060485;  
RA Barrett P., Macdonald A., Helliwell R., Davidson G., Morgan P.J.;  
RT "Cloning and expression of a new member of the melanocyte-stimulating  
hormone receptor family";  
RL J. Mol. Endocrinol. 12:203-213(1994).

CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE  
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE  
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: Z31369; CAA83239.1; -  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC Pfam: PF00001; 7tm\_1; 1.  
CC PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
CC Phosphorylation; Lipoprotein; Palmitate.  
CC DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 38 61 1 (POTENTIAL).  
CC DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 74 97 2 (POTENTIAL).  
CC DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 115 138 3 (POTENTIAL).  
CC DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 156 179 4 (POTENTIAL).  
CC DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 187 211 5 (POTENTIAL).  
CC DOMAIN 212 239 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 240 265 6 (POTENTIAL).  
CC DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 274 297 7 (POTENTIAL).  
CC DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).  
CC CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC LIPID 311 PALMITATE (POTENTIAL).  
SQ SEQUENCE 325 AA; 36584 MW; DE475992BCC4F934 CRC64;

Query Match 55.8%; Score 962.5; DB 1; Length 325;  
Best Local Similarity 59.2%; Pred. No. 5.9e-58;  
Matches 197; Conservative 41; Mismatches 86; Indels 9; Gaps 4;

QY 1 MNSTLQHGMMHTSLHFWRNRSTYQGHGHNATESLGKGYPDGCGYQGFVSPVFTLVGLVISL 60  
Db 1 MNSSFH-----LHFLDLGLNATEGNLS-GLSVRNASSPC-EDMGIAVEVFLALGLISLL 52  
QY 61 ENILVIVATKKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLL-NSTDQAGSFV 119  
Db 53 ENILVIGAIVRNRLHIPMYFFVGLAVADMLVSLNSFWETITVITLLTNKHLVMDASVR 112  
QY 120 NIDNVDSVICSLASCSLLSIADRVFTTFYALQYHINIMTVRRVGIISCIWAACV 179  
Db 113 HDNVFDSVICISVVASMCSLLAIADRVFTTFYALQYHINIMTVRRVGIISCIWAACV 172  
QY 180 SGILFIYSDSTAVIIICLITMFTMLASLYVHMFARLHRIKRIALVPGTGTIRQGA 239  
Db 173 CGTVFIVYESTVYVVVCLIAMFTLLMASLYTHMFLARTHVRRIALPGHSSVRQT 232  
QY 240 NMKGATLTLLIGVFWVWAPFFLFIYFCISQPNVCYCFMSHFNLYLILMCNSIIDP 299  
Db 233 GVKGAITLAMLGLVFIICWAPFFLFIYFCISQPNVCYCFMSHFNLYLILMCNSIIDP 292  
QY 300 LIYALRSQELRTKTFKEIKCYPLGLGLDLSRY 332  
Db 293 LIYALRSQELRTKTFKEIKCYPLGLGLDLSRY 325



[illegible][illegible]

	Matches	176;	Conservative	6;	Mismatches	2;	Indels	0;	Gaps	0;			
Qy	112	TDQSF	TVDNIDNV	DSVIC	SLSLAS	ICSL	SIAD	RYFT	IFYALQ	VHNIMTVRRVG	171		
Db	1	TDQSF	TVDNIDNV	DSVIC	SLSLAS	ICSL	SIAD	RYFT	IFYALQ	VHNIMTVRRVG	60		
Qy	172	CIWAAC	TVSGIL	FIYSD	STAV	IICLT	MEFT	MLAL	MASLYV	HMFELMAR	LHKRIAVLPG	231	
Db	61	CIWAAC	TVSGVLF	FIYSD	SSAV	IICLT	ISMFT	MLVL	MASLYV	HMFELMAR	LHKRIAVLPG	120	
Qy	232	TGTIR	QGNMKG	AITL	TILIG	VVVC	WAPF	FLHL	FIYIS	CPQNPY	CVCFM	SHENLYLILI	291
Db	121	TGTIR	QGNMKG	AITL	TILIG	VVVC	WAPF	FLHL	FIYIS	CPQNPY	CVCFM	SHENLYLILI	180
Qy	292	MCNS	295										
Db	181	MCNA	184										

Search completed: June 4, 2003, 18:16:18  
Job time : 15 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 4, 2003, 18:11:36 ; Search time 52 Seconds  
(without alignments)  
1315.532 Million cell updates/sec

Title: US-09-884-211A-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFNWRSF.....FKRIICCYPLGGICLDSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	1636	94.8	332	11	Q9EQM7	Q9eqm7 mus musculus
2	1490.5	86.4	331	13	O73667	O73667 gallus gall
3	1162.5	67.4	322	13	Q90Y73	Q90y73 takifugu po
4	1162.5	67.4	322	13	Q90VY0	Q90vy0 takifugu ch
5	1157.5	67.1	322	13	Q90Y74	Q90y74 takifugu ra
6	1157.5	67.1	322	13	Q90Y72	Q90y72 takifugu po
7	1115.5	64.6	325	13	O73671	O73671 gallus gall
8	1099	63.7	223	6	Q95LB5	Q95lb5 ovis aries
9	1025.5	59.4	325	13	O93259	O93259 gallus gall
10	823	47.7	314	13	Q90ZP7	Q90zp7 tangara cuc
11	822	47.6	314	13	Q90VY8	Q90vy8 coereba fla
12	821	47.6	314	13	Q90ZQ0	Q90zq0 coereba fla
13	821	47.6	314	13	Q90VX9	Q90vx9 coereba fla
14	818	47.4	314	13	Q90ZP8	Q90zp8 coereba fla
15	818	47.4	314	13	Q90VY8	Q90vy8 coereba fla
16	816	47.3	314	13	Q90ZP9	Q90zp9 coereba fla

17	815	47.2	314	13	Q90W02	Q90w02 coereba fla
18	785	45.5	320	6	Q95MM8	Q95mm8 sus scrofa
19	773.5	44.8	233	6	Q95L18	Q95l18 sus scrofa
20	770.5	44.6	321	6	Q95KV8	Q95kv8 bos taurus
21	769.5	44.6	317	6	O8WMC6	O8wmc6 bos taurus
22	760.5	44.1	317	6	Q95MP3	Q95mp3 equus caball
23	755.5	43.8	317	4	O8WXX6	O8wxx6 homo sapien
24	754.5	43.7	317	4	O9UBF7	O9ubf7 homo sapien
25	754.5	43.7	797	4	O8WUL7	O8wul7 homo sapien
26	753.5	43.7	317	4	O96RU4	O96ru4 homo sapien
27	751.5	43.5	317	4	O8WXX7	O8wxx7 homo sapien
28	749.5	43.4	317	4	Q96I33	Q96i33 homo sapien
29	739	42.8	357	13	O57317	O57317 gallus gall
30	588	34.1	162	6	Q95LB6	Q95lb6 ovis aries
31	573	33.2	221	6	Q9XSH8	Q9xsh8 equus hemio
32	573	33.2	221	6	O9XSH9	O9xsh9 equus klang
33	572	33.1	221	6	O97660	O97660 equus zebra
34	572	33.1	221	6	Q9XSH7	Q9xsh7 equus asinu
35	567	32.9	221	6	Q9XSH6	Q9xsh6 equus grevy
36	520.5	30.2	220	6	O46552	O46552 equus cabal
37	515.5	29.9	220	6	Q9MZA5	Q9mza5 equus cabal
38	438.5	25.4	153	6	O62814	O62814 sus scrofa
39	367.5	21.3	366	13	Q9PU17	Q9pul7 xenopus lae
40	367.5	21.3	366	13	Q9PU16	Q9pul6 xenopus lae
41	362	21.0	364	11	O88584	O88584 mus musculus
42	334.5	19.4	370	13	Q918K8	Q918k8 brachydanio
43	327	18.9	362	13	Q9DDK4	Q9ddk4 brachydanio
44	325.5	18.9	382	11	O9DC35	O9dc35 mus musculus
45	325	18.8	326	6	Q9BF49	Q9bf49 tragelaphus

#### ALIGNMENTS

RESULT 1

ID	Q9EQM7	PRELIMINARY;	PRT;	332 AA.
AC	Q9EQM7:			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Melanocortin-4 receptor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SV;			
RA	Dumont L.M., Wu C.S., Mountjoy K.G.;			
RT	"Characterization of the melanocortin-4 receptor gene.;"			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL; AF201662; AAG35602.1;			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRRHODPSN.			
DR	PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.			
SQ	SEQUENCE 332 AA; 36988 MW; 571708415BD424D3 CRC64;			

Query Match 94.8%; Score 1636; DB 11; Length 332;

Best Local Similarity 94.0%; Pred. No. 2.8e-136;

Matches 312; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MNSTLQHGHTSLHFNWRSFVGQNGATESLGKGYDPGCGYEQLFVSPFVTLGVISLL 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MNSTHHGMYTSLHLNRRSSYGLHSNASESLGKHGPDGCGYEQLFVSPFVTLGVISLL 60

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QY 61 ENILVVAIAKKNKLNHSPWFFTCISLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120
Db 61 ENILVVAIAKKNKLNHSPWFFTCISLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120
QY 121 IDNVDSVICSLLASICSLLSTAVDRYETIFALQYHNIMTVRRVGGIIISCIWAACVTS 180
Db 121 IDNVDSVICSLLASICSLLSTAVDRYETIFALQYHNIMTVRRVGGIIISCIWAACVTS 180
QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLVHMFMLHRIKRIAVLPGTGTROGAN 240
Db 181 GILFIYSDSTAVIICLTMTFMTLMALMASLVHMFMLHRIKRIAVLPGTGTROGAN 240
QY 241 MGKAITLTILIGVVFVWVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
Db 241 MGKAITLTILIGVVFVWVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
QY 301 IYALRSQELRKTFKEIICYPGLGGCLDLSSRY 332
Db 301 IYALRSQELRKTFKEIICYPGLGGCLDLSSRY 332
RESULT 2
073667 PRELIMINARY; PRT; 331 AA.
ID 073667
AC 073667;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Melanocortin 4-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE-LEGHONE; TISSUE=LIVER;
RA Takeuchi S., Takahashi S.;
RT "Molecular cloning of the chicken melanocortin 4-receptor gene widely
RT expressed in peripheral tissues.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB012211; BAA25252.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 331 AA; 36984 MW; 98B25F5A1FFB02C1 CRC64;
Query Match 86.4%; Score 1490.5; DB 13; Length 331;
Best Local Similarity 86.4%; Pred. No. 1.9e-123;
Matches 287; Conservative 16; Mismatches 28; Indels 1; Gaps 1;
QY 1 MNSTLOQHMTSLHFWNRSTYQHGNGATESLGKYPDGGCYEQLFVSPFVTLGLVISLL 60
Db 1 MNFTQHRGTLOPLHFWNQSN-GLHRGASEPSAKHSGCYEQLFVSPFVTLGLISLL 59
QY 61 ENILVVAIAKKNKLNHSPWFFTCISLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 120
Db 60 ENVLVVAIAKKNKLNHSPWFFTCISLAVADMLVSVNSGSETIVITLLNSTDDAQSFVN 119
QY 121 IDNVDSVICSLLASICSLLSIADRYETIFALQYHNIMTVRRVGGIIISCIWAACVTS 180
Db 120 IDNVDSVICSLLASICSLLSIADRYETIFALQYHNIMTVRRVGGIIISCIWAACVTS 179
QY 181 GILFIYSDSTAVIICLTMTFMTLMALMASLVHMFMLHRIKRIAVLPGTGTROGAN 240
Db 180 GILFIYSDSSVVICLLISMEFTMLILMASLVHMFMMHRIKRIAVLPGTGTROGAN 239
QY 241 MGKAITLTILIGVVFVWVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
Db 241 MGKAITLTILIGVVFVWVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 300
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Db 240 MGKAITLTILIGVVFVWVWAPFFLHLFIYISCPNPYCVCFMSHFNLYLILMNCNIIIDPL 299
QY 301 IYALRSQELRKTFKEIICYPGLGGCLDLSSRY 332
Db 300 IYAFRSQELRKTFKEIICCCNLRGLCDLPKY 331
RESULT 3
090Y73 PRELIMINARY; PRT; 322 AA.
ID 090Y73
AC 090Y73;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MCLR.
OS Takifugu porphyreus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176187;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RT gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073677; BAB1733.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35948 MW; A16712C763F91236 CRC64;
Query Match 67.4%; Score 1162.5; DB 13; Length 322;
Best Local Similarity 77.0%; Pred. No. 1.5e-94;
Matches 217; Conservative 31; Mismatches 33; Indels 1; Gaps 1;
QY 39 GCYEQLFVSPFVTLGVISLLENILVIVATAKKNLHSPWFFTCISLAVADMLVSVNSG 98
Db 34 GCYEQLMISTVFLTLGLIISLLENILVVAIVKKNLHSPWFFTCISLAVADMLVSVNSA 93
QY 99 SETIVITLLNS-TDTDAQSFVNIDNVDSVICSLLASICSLLSIADRYETIFALQY 157
Db 94 SETIVIALNSGTLTIPATLIKSDNVDSCSSLASICSLLAIADRYETIFALRY 153
QY 158 HNIMTVRRVGGIIISCIWAACVSGILFIYSDSTAVIICLTMTFMTLMALMASLVHMF 217
Db 154 HNIVTLRRASLVISSTCTVSGVLFIYSESTVLICLTMTFMTLMALMASLVHMF 213
QY 218 MARLHKRIAVLPGTGTROGANMKGATLTILIGVVFVWVWAPFFLHLFIYISCPNPY 277
Db 214 LARLHKRIAMPGNAPIHORANLKGATLTILIGVVFVWVWAPFFLHLILMITCKPNYC 273
QY 278 VCFMSHFNLYLILMNCNIIIDPLIYALRSQELRKTFKEIICC 319
Db 274 TCFMSHFNLYLILMNCNIIIDPLIYAFRSQEMRKTFKEIFCC 315
RESULT 4
090YVO PRELIMINARY; PRT; 322 AA.
ID 090YVO
AC 090YVO;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MCLR.
OS Takifugu chinensis, and
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176185, 31033;
EN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=T.chinensis, and F.rubripes;
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RL gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073675; BAB71731.1; -.
DR EMBL; AB073674; BAB71730.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35975 MW; 8AF03A6371F5E1F6 CRC64;

Query Match 67.4%; Score 1162.5; DB 13; Length 322;
Best Local Similarity 77.0%; Pred. No. 1.5e-94;
Matches 217; Conservative 31; Mismatches 33; Indels 1; Gaps 1;

Oy 39 GCYEQLEFVSPVFTLGLVISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLGLISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTVNIDNVIDSVICSSLLASICSLSIAVDRYFTTFYALQY 157
Db 94 SETIVIALNSGTLTAIPATLIKSMNDVFDMSICSSLLASICSLAIAVDRYITTFYALRY 153

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFL 217
Db 154 HNIVTLRRASLVISISWTCTVSGVLFTIVYSESTVTLICLTMTFTMLMASLYVHMFL 213

Oy 218 MARLHKRIAVLPCTGTIRGANKMGATITLILGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAMPGNAPHQRANLKGAITLTLLGVFVVCWAPFFLHLILMITCPKNPYC 273

Oy 278 VCFMSHENLYLILMCNSIIDPLIYALRSQELRTKFEIICC 319
Db 274 TCFMSHFNMYLILMCNSVIDPIIYAFRSQEMRKTFKEIFCC 315

RESULT 5
Q90Y74
ID Q90Y74 PRELIMINARY; PRT; 322 AA.
AC Q90Y74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu poecilonotus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176185;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RL gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073678; BAB71734.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35945 MW; 1C3F1B3BCED4BFF8 CRC64;

Query Match 67.1%; Score 1157.5; DB 13; Length 322;
Best Local Similarity 76.6%; Pred. No. 4.1e-94;
Matches 216; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

Oy 39 GCYEQLEFVSPVFTLGLVISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLGLISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTVNIDNVIDSVICSSLLASICSLSIAVDRYFTTFYALQY 157
Db 94 SETIVIALNSGTLTAIPATLIKSMNDVFDMSICSSLLASICSLAIAVDRYITTFYALRY 153

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFL 217
Db 154 HNIVTLRRASLVISISWTCTVSGVLFTIVYSESTVTLICLTMTFTMLMASLYVHMFL 213

Oy 218 MARLHKRIAVLPCTGTIRGANKMGATITLILGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAMPGNAPHQRANLKGAITLTLLGVFVVCWAPFFLHLILMITCPKNPYC 273

Oy 278 VCFMSHENLYLILMCNSIIDPLIYALRSQELRTKFEIICC 319
Db 274 TCFMSHFNMYLILMCNSVIDPIIYAFRSQEMRKTFKEIFCC 315

RESULT 5
Q90Y74
ID Q90Y74 PRELIMINARY; PRT; 322 AA.
AC Q90Y74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu radiatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176186;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RL gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073676; BAB71732.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35917 MW; 37A8339FDCD84C38 CRC64;

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Query Match 67.1%; Score 1157.5; DB 13; Length 322;
Best Local Similarity 76.6%; Pred. No. 4.1e-94;
Matches 216; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

Oy 39 GCYEQLEFVSPVFTLGLVISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLGLISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTVNIDNVIDSVICSSLLASICSLSIAVDRYFTTFYALQY 157
Db 94 SETIVIALNSGTLTAIPATLIKSMNDVFDMSICSSLLASICSLAIAVDRYITTFYALRY 153

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFL 217
Db 154 HNIVTLRRASLVISISWTCTVSGVLFTIVYSESTVTLICLTMTFTMLMASLYVHMFL 213

Oy 218 MARLHKRIAVLPCTGTIRGANKMGATITLILGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAMPGNAPHQRANLKGAITLTLLGVFVVCWAPFFLHLILMITCPKNPYC 273

Oy 278 VCFMSHENLYLILMCNSIIDPLIYALRSQELRTKFEIICC 319
Db 274 TCFMSHFNMYLILMCNSVIDPIIYAFRSQEMRKTFKEIFCC 315

RESULT 6
Q90Y72
ID Q90Y72 PRELIMINARY; PRT; 322 AA.
AC Q90Y72;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Melanocortin receptor-1.
GN MC1R.
OS Takifugu poecilonotus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=176188;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunimoto M., Mizukami Y.;
RT "Discrimination of Takifugu species based on melanocortin receptor-1
RL gene nucleotide sequence.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073678; BAB71734.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35945 MW; 1C3F1B3BCED4BFF8 CRC64;

Query Match 67.1%; Score 1157.5; DB 13; Length 322;
Best Local Similarity 76.6%; Pred. No. 4.1e-94;
Matches 216; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

Oy 39 GCYEQLEFVSPVFTLGLVISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVSNG 98
Db 34 GCYEQMLISTEVFTLGLISLLENILVVAIAKKNLHSPMYFFICS LAVADMLVSVNA 93

Oy 99 SETIVILLNS-TDTDAQSTVNIDNVIDSVICSSLLASICSLSIAVDRYFTTFYALQY 157
Db 94 SETIVIALNSGTLTAIPATLIKSMNDVFDMSICSSLLASICSLAIAVDRYITTFYALRY 153

Oy 158 HNIMTVRRVGIISCIWAACVSGILFTIYSDSTAVIICLTMTFTMLMASLYVHMFL 217
Db 154 HNIVTLRRASLVISISWTCTVSGVLFTIVYSESTVTLICLTMTFTMLMASLYVHMFL 213

Oy 218 MARLHKRIAVLPCTGTIRGANKMGATITLILGVFVVCWAPFFLHLIFVISCQPNPYC 277
Db 214 LARLHMKRIAMPGNAPHQRANLKGAITLTLLGVFVVCWAPFFLHLILMITCPKNPYC 277

Oy 278 VCFMSHENLYLILMCNSIIDPLIYALRSQELRTKFEIICC 319
Db 274 TCFMSHFNMYLILMCNSVIDPIIYAFRSQEMRKTFKEIFCC 315

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Db 214 LARLHMKRIAAMPNGAPIHQORANLKGAIITLILGVFVVCWAPFFLLHILMITCPKNPYC 273
Qy 278 VCFMSHNVLXILIMCNSIIDPLIYALRSQELRKTKEIICC 319
Db 274 TCFMSHNMYLILIMCNSVIDPIIYAPRSQEMRKTKEIFCC 315

RESULT 7
073671
ID 073671 PRELIMINARY; PRT; 325 AA.
AC 073671;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Melanocortin 5-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=LIVER;
RA Takeuchi S., Takahashi S.;
RT "Cloning and expression of the chicken melanocortin 5-receptor gene.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB012868; BAA25840.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 325 AA; 36994 MW; 35441907C71E4FA2 CRC64;

Query Match 64.6%; Score 1115.5; DB 13; Length 325;
Best Local Similarity 65.3%; Pred. No. 2.1e-90;
Matches 215; Conservative 46; Mismatches 59; Indels 9; Gaps 4;

Qy 9 MHTSLHF----NRSTYGHGNATESLKGYPGGCYEQLFVSPEVFTLGVISLLENIL 64
Db 1 MNTSSQLYSELNLSAFSGNFTVPTVKSSSP--C-EQVVIAAEVFLILGVISLLENIL 56
Qy 65 VIVAIKNNLHSPMVFYFFCISLAVADMLYSVNSGETIVITLNSDTHDAQ-SFTVNIDN 123
Db 57 VICAIKNNLHSPMVFYFFCISLAVADMLYSVNSGETIVITLNNRHIIIMEDAFVRHIDN 116
Qy 124 VIDSVICSSILASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIISCIWAACVTSVGI 183
Db 117 VFDSLICISVWASCSLLAIAVDRIYIFVALRYHNIMTVKRSGLLIACIWTFTCCGII 176
Qy 184 FIYSDSTAVITCLITMFTMLMALMASLYVHMFLMARLHKRIAVLPCTGTIROGANNMGK 243
Db 177 FIIYESTVVIICLITMFTMLFLMVSIVHFLMARLHARTHVKKIAALPGYNSVHQRTSMKG 236
Qy 244 AITLTILGVFVVCWAPFFLHILFISCPNQPCVCFMSHFNLYLILIMCNSIIDPLIYA 303
Db 237 AITLTMLLGIIVCWAPFFLHILFISCPNQPCVCFMSHFNLYLILIMCNSVIDPLIYA 296
Qy 304 LRSQELRKTKEIICCYPLGGLCLSSRY 332
Db 297 FRSQENRKTKEIICCYSRVMVCGLSNKY 325

RESULT 8
095LB5
ID 095LB5 PRELIMINARY; PRT; 223 AA.
AC 095LB5;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Melanocortin-4 receptor (Fragment).
GN MC4-R.
OS Ovis aries (Sheep).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21421436; PubMed=11530231;
RA Iqbal J., Pompolo S., Dumont L.M., Wu C., Mountjoy K.G., Henry B.A.,
RA Clarke I.J.;
RT "Long-term alterations in body weight do not affect the expression of
RT melanocortin receptor-3 and -4 mRNA in the ovine hypothalamus.";
RL Neuroscience 105:931-940(2001).
DR EMBL; AF345913; AAL27186.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
KW NON_TER 1
FT NON_TER 223
FT NON_TER 223
SQ SEQUENCE 223 AA; 24542 MW; C8EBB5EBCAB766E CRC64;

Query Match 63.7%; Score 1099; DB 6; Length 223;
Best Local Similarity 96.0%; Pred. No. 4e-89;
Matches 214; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 82 FICSLAVADMLYSVNSGETIVITLNSDTHDAQSFVNIDNVIDSVICSSLLASICSLL 141
Db 1 FICSLAVADMLYSVNSGETIVITLNSDTHDAQSFVNIDNVIDSVICSSLLASICSLL 60
Qy 142 STAVDRYFTIFVALQYHNIMTVRRVGIISCIWAACVTSVGIIFYSIDSTAVIICLITMF 201
Db 61 STAVDRYFTIFVALQYHSINTYRVVAITISAIWAACVTSVGIIFYSIDSSAVIICLITVF 120
Qy 202 FTMLMALSYVHMFLMARLHKRIAVLPCTGTIROGANNMGKAITILIGVFWVCWAPF 261
Db 121 FTMLMALSYVHMFLMARLHKRIAVLPCTGTIROGANNMGKAITILIGVFWVCWAPF 180
Qy 262 FLHLFIYISCPNQPCVCFMSHFNLYLILIMCNSIIDPLIYAL 304
Db 181 FLHLFIYISCPNQPCVCFMSHFNLYLILIMCNSVIDPLIYAL 223

RESULT 9
093259
ID 093259 PRELIMINARY; PRT; 325 AA.
AC 093259;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Melanocortin 3-receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=99144114; PubMed=9990303;
RA Takeuchi S., Takahashi S.;
RT "A possible involvement of melanocortin 3-receptor in the regulation
RT of adrenal gland function in the chicken.";
RL Biochim. Biophys. Acta 1448:512-518(1999).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB017137; BAA32555.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
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Db	14	SNASEGNSHVNATVAGGWCQG-----LDIPNELFLALGSLVLENLLVVAAILKNRNH	68
Qy	77	SPMYFFICSLAVADMLVSVNSGSETIVITLL-NSTDDTAQSETVNDINVIDSVICSSLLA	135
Db	69	SPTYVFFICCLAVSDMLVSVISNLAELMFLMLLGEHVLVMRPSIVRHMDSVIDFLICSSVVS	128
Qy	136	SICSILSLTAVDRYETIFALLOYHNIMTVRRVGIIISCSITWAACITVSGILFIIVYSDSTAVII	195
Db	129	SLSLGLGVJAVDRYITIFALRYHSLIMTIQRAVVTWASVLMSTVSLVLIAYRNTILL	188
Qy	196	CLITMFTMLMALMSLVYHMFMLRKRIKIAVLPGTGTIRQANNKGAITITLILIGVFF	255
Db	189	CLIGFFFLMLVMLVLYIHMFLARHRLHSISSQQKPPTAHRGGSILKGAVLTILLGVFF	248
Qy	256	VCWAPFFLHLIFYTSCPONPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQELKRTKE	315
Db	249	ICWGPFFHLLIIVTCTPNPECACFFSYFNLFLLIILICNSVIDPLIYAFRSQELARTLRE	308
Qy	316	IIOC 319	
Db	309	VWTC 312	

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RESULT 12
Q90ZQ0 PRELIMINARY; PRT; 314 AA.
ID Q90ZQ0
AC Q90ZQ0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Melanocortin 1 receptor.
OS Coereba flaveola (bannaquait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Coereba.
NCBI_TaxID=87177;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21261843; PubMed=11369199;
RA Theron E., Hawkins K., Bermingham E., Ricklefs R.E., Mundy N.I.;
RT "The molecular basis of an avian plumage polymorphism in the wild: a
RT melanocortin-1-receptor point mutation is perfectly associated with
RT the melanic plumage morph of the bananaquit, Coereba flaveola.";
RL Curr. Biol. 11:550-557(2001).
DR EMBL; AF362584; AAK50791.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 34998 MW; 2174CD2BB615BAEB CRC64;

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DB      249 ICWGFFHHLLIVTCTPNFCACFSYFNFLIICNSVIDPLIYAFRSQELRRLTRE 308
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QY      316 IICC 319
        ::|
DB      309 VVTC 312
PRELIMINARY;          PRT;    314 AA.

RESULT 13
Q90VX9
ID Q90VX9
AC Q90VX9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Melanocortin 1 receptor.
OS Coereba flaveola (bannaquitt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Emberizinae; Coereba.
NCBI TAXID=87177.

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RESULT 14
Q902P8
ID Q902P8 PRELIMINARY; PRT; 314 AA.
AC Q902P8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 10:15:58 ; Search time 76 seconds  
(without alignments)  
8009.913 Million cell updates/sec

Title: US-09-884-211a-2

Perfect score: 1985

Sequence: 1 ctaagaccggtggaggagcag.....gaaataaaaaaaaaaaaaa 1985

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	958.2	48.3	1671	2	US-08-662-560-1
2	958.2	48.3	1671	2	US-08-780-749A-5
3	958.2	48.3	1671	4	US-08-870-511-5
4	939	47.3	1671	3	US-08-706-281A-15
5	939	47.3	1671	4	US-09-097-231-15
6	817.4	41.2	996	1	US-08-671-525B-7
7	817.4	41.2	996	1	US-08-672-109B-7
8	817.4	41.2	996	1	US-08-842-045-7
9	817.4	41.2	996	2	US-08-842-238-7
10	817.4	41.2	996	3	US-08-629-335B-7
11	815.6	41.1	999	4	US-08-870-511-7
12	815.6	41.1	999	4	US-08-870-511-9
13	815.6	41.1	999	4	US-08-870-511-11
14	426.2	21.5	975	1	US-08-671-525B-9
15	426.2	21.5	975	1	US-08-672-109B-9
16	426.2	21.5	975	1	US-08-842-045-9
17	426.2	21.5	975	2	US-08-842-238-9
18	426.2	21.5	975	3	US-08-629-335B-9
19	426	21.5	978	3	US-08-706-281A-17
20	424.8	21.4	978	4	US-09-097-231-17
21	424.8	21.4	1650	4	US-08-387-805-15
22	396.6	20.0	1080	1	US-08-671-525B-5
23	396.6	20.0	1080	1	US-08-672-109B-5
24	396.6	20.0	1080	1	US-08-842-045-5
25	396.6	20.0	1080	2	US-08-842-238-5
26	396.6	20.0	1080	3	US-08-629-335B-5
27	389	19.6	1338	2	US-08-044-812A-3

Sequence 3, Appli  
Sequence 3, Appli  
Sequence 11, Appli  
Sequence 11, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 3, Appli  
Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
US-08-662-560-1  
; Sequence 1, Application US/08662560  
; Patent No. 5908609  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank  
; APPLICANT: Huszar, Dennis  
; APPLICANT: Wei, Gu  
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS  
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/662,560  
; FILING DATE: 10-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-060  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1671 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 394...1389  
; OTHER INFORMATION:  
US-08-662-560-1

Db	1108	GCCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1167
Qy	1221	GCTCCATCTTCTCCACCTTGATATCTACATCTCTTGTCGCCAGAAATCCATCTGCTG	1280
Db	1168	GCCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1227
Qy	1281	TGCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1340
Db	1228	TGCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1287
Qy	1341	CCCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1400
Db	1288	CCCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1347
Qy	1401	TGCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1460
Db	1348	TGCTTCAATGAGGAGCGATTACCTTGACCATCTGATTGGCTCTTTGTTGCTGCTGG	1407
Qy	1461	GTACTAAA--AACATGCACACAGAGCTTCTTCAATCTGATCATGTTGAATCCATCTG	1518
Db	1408	GCAATATAGGAACATGATATGATGATGATGATGATGATGATGATGATGATGATGATG	1467
Qy	1519	GGCAACAGCTGCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG	1578
Db	1468	CTGCAACAGCTTCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG	1526
Qy	1579	ACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1637
Db	1527	AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1581
Qy	1638	ATGCTAC--TTTTGGGCTGTCATGTTAATCCAT--TTCGACGCTGTAGACACTTTTCAAT	1695
Db	1582	ATGCTACTTTTGGCCATAAATATGATGATGATGATGATGATGATGATGATGATGATGATG	1641
Qy	1696	TCTAGAAAAAGAA 1708	
Db	1642	TACAAAAAGAAAA 1654	

RESULT 2

US-08-780-749A-5

; Sequence 5, Application US/08780749A

; Patent No. 5932779

; GENERAL INFORMATION:

; APPLICANT: Lee, Frank

; APPLICANT: Huszar, Dennis

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS

; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/780,749A

; FILING DATE: 08-JAN-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Laura A. Coruzzi

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

[illegible]



```

; APPLICATION NUMBER: US/08/706,281A
; FILING DATE: 04-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6100048nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1671 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..393
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 394..1389
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1390..1671
US-08-706-281A-15

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Query Match 47.3%; Score 939; DB 3; Length 1671;  
Best Local Similarity 79.4%; Pred. No. 2.9e-219;  
Matches 1249; Conservative 0; Mismatches 304; Indels 2

[illegible]

RESULT 5  
US-09-097-231-15  
; Sequence 15, Application US/09097231  
; Patent No 6278038





Db 1468 CTGCAACAGCTTTCTCTTCCTGTPAGGTACTGTGTTGAG-ATATCCATTGTGTAATTTA 1526  
QY 1579 ACTTTATGATGTTTGTGATGTGAAAAAATGCCAGGCTCTGTA-CATTGCTAAATGTC 1637  
Db 1527 AGCCTATGATTTT-ATGAGAAAAATGCCAGTCTCTGATATTATTTCAATCTC 1581  
QY 1638 ATGCTAC-TTTTGGGCTGTGCTTTTAAATCCAT-TTCGAGGCTGTAGACACTTTGAATT 1695  
Db 1582 ATGCTACTTTTGGCCATAAAATATCAATCTATGTTATAGTTGTAGGCACTGTGGATT 1641  
QY 1696 TCTAGAAAAGAAA 1708  
Db 1642 TACAAAAAGAAAA 1654

## RESULT 6

US-08-671-525B-7  
; Sequence 7, Application US/08671525B  
; Patent No. 5703220  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: June 27, 1996  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600

TELEFAX: (810)641-0270

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 996 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 1..996

US-08-671-525B-7

Query Match 41.2%; Score 817.4; DB 1; Length 996;

Best Local Similarity 89.3%; Pred. No. 9.3e-190;

Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 455 CACCCTTCAGCAGGATGACACTTCTCTCCACTTCTGGAACGGCAGCCTACGGACA 514

Db 9 CTCACCCACCGTGGGATGCACACTTCTGCACTCTGGAACGGCAGCAGTTACAGACT 68

QY 515 GCAGGCAACGCCACTGAGTCCCTTGGCAAGGCTACCCCGACGGGATGCTACGAGCA 574

Db 69 GCACGCAATGCCAGTGAGTCCCTTGGAAAAAGGCTACTCTGATGAGGGTCTACGAGCA 128  
QY 575 ACTCTTCGTCTCCCGGAGGTGTCGTGACTCTCTGGGGTCTAAGACTTCTGCTGGAGACAT 634  
Db 129 ACTTTTGTCT 188  
QY 635 TCTGGTATCGTGCAATAGCCAAAGAACTCTGCACATCACCCTCATCTGACTTCTTTCAT 694  
Db 189 CTTAGTATTTGGCATATAGCCAAAGAACTCTGCAATCACCCTCATCTTTCAT 248  
QY 695 CTGTAGCCTGGCTGTGCCGATATGCTGGTGGAGGTTTCCAAACGGGTCAGAGACCATCGT 754  
Db 249 CTGCAGCTTGGCTGTGGCTGATATGCTGGTGGAGGTTTCAAATGATGATGATATAT 308  
QY 755 CATCACCTCTTTGAACAGTACGGATACGGAGCCGACAGTTTTCAGGTGATATATGATAA 814  
Db 309 CATCACCTATTAACAGATACAGATACGGATGACAGAGTTTTCAGGTGATATATGATAA 368  
QY 815 TGTATTGACTCGGTGATCTGTAGTCTCTTCTGCTCGCTCGATTTGCGAGCCTGCTCTCAAT 874  
Db 369 TGTATTGACTCGGTGATCTGTAGTCTCTTCTGCTCGATTTGCGAGCCTGCTCTCAAT 428  
QY 875 TGCAGTGGACAGGTACTTTTACTATCTTTATGCCCCCAGTACCATAACATCATGACGGT 934  
Db 429 TGCAGTGGACAGGTACTTTTACTATCTTCTATGCTCTCCAGTACCATAACATCATGACGT 488  
QY 935 GAGCGGGTGGGATCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994  
Db 489 TAAGCGGGTGGGATCATCATCAAGTTGATCTGGGAGCTTGGCAGGTTTCAGGCAATTT 548  
QY 995 GTTCATCATTTACTCGGACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054  
Db 549 GTTCATCATTTACTCAGATAGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608  
QY 1055 CATGCTGGCCCTCATGCTTCTCTCTAGTCCACATGTTCTCATGCGCCAGCAGATGACAT 1114  
Db 609 CATGCTGGCTCTCATGCTTCTCTCTATGCTCCACATGTTCTGATGGCCAGGCTTCACAT 668  
QY 1115 CAAGAGAAATGCCGCTCTCCCGGACCGGACCATCCGCCAAGGGCCCAACATCAAGGG 1174  
Db 669 TAAGAGGATGCTGCTCTCCCGGACCTGGTGCCATCCGCCAAGGTGCCAATATGAAGGG 728  
QY 1175 TGCCATTACCTTGACCATACTCATTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1234  
Db 729 AGCGATTACCTTGACCATCTGATTTGGGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 788  
QY 1235 CCAGTTGATATTCATATCTCTTCTCCCGAAGTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1294  
Db 789 CCAGTTAATATTCATATCTCTTCTCTCAGAAATCCCATATTTGCTGCTGCTGCTGCTGCT 848  
QY 1295 CTTTAACTTGTACCTCATTTCTGATCATGTGTAACCTCCATCATCCAGCCTCTCATTTATGC 1354  
Db 849 CTTTAACTTGTATCTCATCTACTGATCATGTGTAATTCATTCATCATGCTCTGATTTATGC 908  
QY 1355 ACTCCGGAGCAAGAGCTGAGGAAAACTTCAAAGAGATCATCTGTTGCTATCTCTGCTGG 1414  
Db 909 ACTCCGGAGTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTTGCTATCTCTGCTGG 968  
QY 1415 TGGCCTTTGTGACTTGTCTAGCAGATA 1441  
Db 969 AGGCCTTTGTGACTTGTCTAGCAGATA 995

## RESULT 7

us-08-672-109B-7

; Sequence 7, Application US/08672109B

; Patent No. 5710265

; GENERAL INFORMATION:

; APPLICANT: Yamada, Tadataka

; APPLICANT: Gantz, Ira

; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,109B  
; FILING DATE: June 27, 1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 996 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..996  
; US-08-672-109B-7

Query Match 41.2%; Score 817.4; DB 1; Length 996;

Best Local Similarity 89.3%; Pred. No. 9.3e-190;  
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY	455	CACCTTTCACGACGGAATACACACTTCTCTCCACTTCTGGAACCGCAGCACCTAGGACA	514
Db	9	CTCCACCCACCGTGGGATGCACACTCTCTGCACCTCTGGAACCGCAGGTACAGACT	68
QY	515	GCACGGCAAGCCACTAGTCCCTTGGCAAGGCTACCCCGACGGGGGATGTACGAGCA	574
Db	69	GCACAGCAATGCCAGTGGTCCCTTGGAAAGGCTACTCTGATGGAGGGTGTACGAGCA	128
QY	575	ACTCTTCGTCCTCCCGAGGTCTGTGACTCTGGGGTCATAAGCTTCTCTGGAGAACAT	634
Db	129	ACTTTTGTCTCTCTCTGAGGTGTGTGACTCTGGGTGTCATCAGCTTGTGGAGAAAT	188
QY	635	TCTGTGTGTCGTGGCAATAGCAAGAACAAAGTCTGCACCTCACCCATGTACTTTTCAT	694
Db	189	CTTAGTGTGTTGGCAATAGCAAGAACAAAGTCTGCATTCACCCATGTACTTTTCAT	248
QY	695	CTGTAGCCCTGGCTGGCCGATATGCTGGTAGCGTTTCCACGGGTGACAGACCATCGT	754
Db	249	CTGCAGCTGGCTGGCTGGCTGGATGCTGGTAGCGTTTCAATGGATCAGAAACCATTA	308
QY	755	CATCACCTTGTGAACAGTACGATACGACCGCAGAGTTTTCACGGTGAATATTGATAA	814
Db	309	CATCACCTTATTAACAGTACAGATACGATACGATACGATACGATGAAATATTGATAA	368
QY	815	TGTCATTGACCTGGTGTATCTGTAGCTCTTGTCTGCCTCGCAATTTTCAGCCCTCTCAAT	874
Db	369	TGTCATTGACCTGGTGTATCTGTAGCTCTTGTCTGCCTCGCAATTTTCAGCCCTCTCAAT	428
QY	875	TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCTCCAGTACCATACATCAACGGT	934

Db	429	TGCAGTGGACAGGTACTTTTACTATCTTCTATGCTCTCCAGTACCAATAACATTATGACAGT	488
QY	935	GAGGCGGGTTGGATCATCATCATCAGTTGCTATGCGGGGCTTGCACGGTGTACAGGCATCTT	994
Db	489	TAGCGGGTTGGATCATCATCATCAGTTGCTATGCGGGGCTTGCACGGTGTACAGGCATCTT	548
QY	995	GTTTCATCATTTTACTCGGACAGTACTGCTGTATCATCATCTGCCTCATCACCATTGTTCTTAC	1054
Db	549	GTTTCATCATTTTACTCGATAGTAGTGTCTGTATCATCTGCCTCATCACCATTGTTCTTAC	608
QY	1055	CATGTGGCCCTCATCGGCTTCTCTCTACCTGCACATGTTCTCTCATGGCCAGACTGACAT	1114
Db	609	CATGTGGCTCTCATGGCTTCTCTCTATGTCACATGTTCTCTGATGGCCAGGCTTCACAT	668
QY	1115	CAAGAGATCGCGCTCTCCCGGACCGGACCATCCGCCAAGGGGCCAACATGAAGG	1174
Db	669	TAGAGGAGTGTCTCTCCCGGACCTGTTGCCATCCGCCAAGGTGCGCAATGAAGG	728
QY	1175	TGCCATTACCTTGACCATCTCATTTGGGCTCTTTCGTCGTCGTCGTCGTCCTCTCTCT	1234
Db	729	AGGATTACCTTGACCATCTCTGTTGGGCTCTTTCGTCGTCGTCGTCCTCTCTCTCT	788
QY	1235	CCACTTGATATCTACATCTCTTGTGCCAGAAATCATCTGTGTGTGTGTGTGTGTGTGTGT	1294
Db	789	CCACTTAATATCTACATCTCTTGTCTCAGAAATCATCTGTGTGTGTGTGTGTGTGTGTGT	848
QY	1295	CTTTAACTTGTACCTCATCTCATGTCATGTAACCTTCAAGAGATCATCTGTGTGTGTGTGTGT	1354
Db	849	CTTTAACTTGTATCTCATCTCATGTCATGTAATCAATCATCGATCTCTGTGTGTGTGTGTGT	908
QY	1355	ACTCGGAGCCAGAGCTGAGGAAACCTTCAAGAGATCATCTGTGTGTGTGTGTGTGTGTGTGT	1414
Db	909	ACTCGGAGCTCAAGAACTGAGGAAACCTTCAAGAGATCATCTGTGTGTGTGTGTGTGTGTGT	968
QY	1415	TGGCCTTGTGTACTGT	1441
Db	969	AGGCTTGTGTACTGT	995

RESULT 8

US-08-842-045-7  
; Sequence 7, Application US/08842045  
; Patent No. 5817787  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; APPLICANT: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/842,045  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:

Qy	455	CACCC	TTACG	ACGGA	ATGCAC	ATTCTCT	CACATTCT	TGGA	CCGCG	CAGC	ACCTT	CACG	GACA	514	
Db	9	CTCC	ACCC	ACCG	TGGG	ATGCAC	ATTCTCT	CGCA	CTCT	CGCA	CTCT	TGGA	CCGCG	ACAG	515
Qy	515	GCAC	GGCA	CCG	CAC	T	CAG	TCC	TTG	CA	AA	G	GTAC	CCG	516
Db	69	GCAC	GCA	AA	TG	CCAG	T	GG	GG	CT	CT	CG	AA	GG	128
Qy	575	ACT	TT	CG	T	CT	CC	CG	G	A	G	T	GT	CG	576
Db	129	ACT	TT	TT	TT	CT	C	CT	C	CT	G	GT	GT	GT	188
Qy	635	TC	TG	GT	G	T	A	T	C	G	A	A	T	C	636
Db	189	CT	T	A	G	T	G	A	T	T	G	G	C	A	248
Qy	695	CT	G	T	A	G	C	T	G	G	C	T	A	T	696
Db	249	CT	G	A	G	C	T	T	G	G	C	T	A	T	308
Qy	755	CAT	C	A	C	C	C	T	T	G	A	C	A	G	756
Db	309	CAT	C	A	C	C	C	T	A	T	A	A	C	A	368
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Db	369	TG	C	A	T	T	A	G	C	T	G	T	A	G	428
Qy	875	TG	C	A	G	T	G	G	A	C	A	G	T	A	876
Db	429	TG	C	A	G	T	G	G	A	C	A	G	T	A	488
Qy	935	G	A	G	C	G	G	T	T	G	G	A	C	A	936
Db	489	T	A	A	C	G	G	T	T	G	G	A	C	A	548
Qy	995	G	T	T	C	A	T	A	T	T	A	G	T	A	1054
Db	549	G	T	T	C	A	T	A	T	T	A	G	T	A	608
Qy	1055	C	A												

[illegible]

Qy		575	ACTCTTCGTCTCCCGGAGGTGTTCTGTA	634
Db		129	ACTTTTGTCTCTCCTGAGGTGTTGTGACT	188
Qy		635	TCTGGTGATCGTGGCAATAGCAAGAACA	694
Db		189	CTTAGTGATTGTGGCAATAGCAAGAACA	248
Qy		695	CTGTAGCCTTGGCTGTGGCCGATATGCT	754
Db		249	CTGCAGCTTGGCTGTGGCTGATATGCT	308
Qy		755	CATCACCCCTGTTGAACAGTACGGATAC	814
Db		309	CATCACCCCTATTAAACAGTACAGATAC	368
Qy		815	TGTCATTGACTCGGTGATCTGTAGTCT	874
Db		369	TGTCATTGACTCGGTGATCTGTAGTCT	428
Qy		875	TGCAGTGGACAGGTFACCTTTACTATCT	934
Db		429	TGCAGTGGACAGGTFACCTTTACTATCT	488
Qy		935	GAGCGGGTTGGGATCATCATCAGTTGCC	994
Db		489	TAAGCGGGTTGGGATCATCATCAGTTGC	548
Qy		995	GTTTCATCATTTACTCGGACACAGTACT	1054
Db		549	GTTTCATCATTTACTCAGATAGTAGTGT	608
Qy		1055	CATGCTGGCCCTCATGGCTTCTCTCTAC	1114
Db		609	CATGCTGGCTCTCATGGCTTCTCTCTAT	668
Qy		1115	CAGAGAAATCGCGTCTCTCCGGGACCG	1174
Db		669	TAAGAGATTGCTGTCTCTCCCGGCACT	728
Qy		1175	TGCGATTACCTTGACCATACTCATTTGG	1234
Db		729	AGCGATTACCTTGACCATACTCATTTGG	788
Qy		1235	CGACTTGATATTCTACATCTTGTGTCCC	1294
Db		789	CCAATTAAATTTCTACATCTTGTGTCCC	848
Qy		1295	CTTTAACTTGTACTCATCTTGATCATGT	1354
Db		849	CTTTAACTTGTATCTCATCTGATCATGT	908
Qy		1355	ACTCCGAGGCCAAGAGCTGAGGAAAAC	1414
Db		909	ACTCCGAGGTCAGAAGCTGAGGAAAAC	968
Qy		1415	TGGCCTTTGTGACTTGTCTAGCAGATA	1441
Db		969	AGGCGCTTTGTGACTTGTCTAGCAGATA	995

STREET: P.O. Box 828  
CITY: Bloomfield Hills  
STATE: MI  
COUNTRY: US  
ZIP: 48303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/629,335B  
FILING DATE: July 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, DeAnn F.  
REGISTRATION NUMBER: 36683  
REFERENCE/DOCKET NUMBER: 2115-000853DVA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810)641-1600  
TELEFAX: (810)641-0270  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 996 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..996  
US-08-629-335B-7

Query Match 41.2%; Score 817.4; DB 3; Length 996;  
Best Local Similarity 89.3%; Pred. NO. 9.3e-190;  
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

	Qy	455	CACCCTTTGACGACGGAAATGCACACTTCTCCACTTCGTGGAAACCGAGCACCTACGGACA	514
	Db	9	CTCCACCCACCGTGGGATGCACACTTCTTGCACTCTGGAAACCGCAGCATACAGACT	68
	Qy	515	GCACGGAAACGCCACTGAGTCCCCTTGGCAAAGGCTACCCGACGGGGATGCTACGAGCA	574
	Db	69	GCACAGCAATGCCAGTAGTCCCTTGGAAAAGGCTACTCTGATGGAGGGTGTACGAGCA	128
	Qy	575	ACTCTTCGTCTCCCCGGAGGTGTTCGTGACTCTCTGGGGGTCTAAGCTTTGCTGGAGAACAAT	634
	Db	129	ACTTTTGTCTCTCCTCAGGTGTTTTGTGACTCTGGGTGTCTATCAGCTTTGTTGGAAATAAT	188
	Qy	635	TCTCGTGATCGTGGCAATAGCAACGAAGAATCTGCACATCACCCATGTACTTTTTCAT	694
	Db	189	CTTAGTGATTGGCAATAGCAACGAAGAATCTGCATTCACCCATGTACTTTTTCAT	248
	Qy	695	CTGTAGCCTTGGCTCTGGCCGATATGCTGGTGAGCGTTTTCCAACGGGTTCAGAGACCATCGT	754
	Db	249	CTGCAGCTTGGCTCTGGCTGATATGCTGGTGAGCGTTTTCAAATGGATCAGAAACCATTAAT	308
	Qy	755	CATCACCCCTGTTGAACAGTACGGATACGGAGCGGCAGAGTTTCACGGTGAATATTGTATAA	814
	Db	309	CATCACCCCTATTAAACAGTACAGATACGGATTGCACAGAGTTTCACAGTGAATATTGTATAA	368
	Qy	815	TGTCATTGTACTCGGTGATCTGTAGTCTCCCTTGTGCGCTTCGATTTCACGCGCTGCTCTCAAT	874
	Db	369	TGTCATTGTACTCGGTGATCTGTAGTCTCCCTTGTGCAATTCCTGACGCGCTGCTTCAAT	428
	Qy	875	TGCAGTGGACAGGTACTTTTACTATCTTTTATGCGCCTCCAGTACCAATAACATCATGACGGT	934
	Db	429	TGCAGTGGACAGGTACTTTTACTATCTTTTATGCTCTCCAGTACCAATAACATPATCAGACT	488



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; CURRENT FILING DATE: 1997-06-06
;
; NUMBER OF SEQ ID NOS: 45
;
; SOFTWARE: Patent In Ver. 2.0
;
; SEQ ID NO 9
;
; LENGTH: 999
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: (1)..(996)
;
; US-08-870-511-g

```

Query Match	41.1%	Score 815.6;	DB 4;	Length 999;
Best Local Similarity	89.0%	Pred. NO. 2.5e-189;		
Matches 881; Conservative	0;	Mismatches 109;	Indels	0

455	QY	CACCC	TTACGACGGAA	TGCACACTTCTCTCCACTTCTGGAACCGCAGCACCTTACGGACA	514
9	Db				
9	CTCCAC	CCACCGTGGGATGCACACTTCTCTGCACCTCTGGAACCGCAGCAGTTACACACT	68		
515	QY	GCACGG	CACGCCACTCAGTCCCTTGCCAAAGGCTACCCGACGGGGGATGCTACGAGCA	574	
69	Db	GCACAG	CAATGCCAGTGAGTCCCTTGAAAGGCTACTCTGATGGAGGGTGCCTACGAGCA	128	
575	QY	ACTCTTC	CGTCCCCCGGAGGTGTTCTGTGACTCTGGGGGTCTAATAGCTTGTCTGGAGAACAT	634	
129	Db	ACTTTT	TGCTCTCCTCGAGGTGTTGTGACTCTGGGTGTCTCAGCTGTGTTGGAGATAT	188	
635	QY	TCGTGT	GATCGTGGCAATAGCCAAAGAACAGAATCTGCATCACCCCATGTACTTTTCAT	694	
189	Db	CTTAGT	GTGTGGCAATAGCCAAAGAACAGAATCTGCATTCACCCATGTACTTTTTCAT	248	
695	QY	CTGTAG	CGCTGGCGCATATGCTGGTGAGCGTTTCCAAAGGGTTCAGAGACCATCGT	754	
249	Db	CTCAG	TGGCTGTATGCTGGTGAGCGTTTCAATTTGGATTCAGAAACCATATAT	308	
755	QY	CATCAC	CCCTGTTGAAACAGTACGGATACGGACGCGCAGAGTTTCACGGTGAATATTGTAA	814	
309	Db	CATCAC	CCCTATTAAACAGTACAGATATGGATGCACAGAGTTTCACAGTGAATATTGTAA	368	
815	QY	TGTCAT	TGACTCGGTGATCTGTAGTCTCTGCTCGCTCGATTTGGAGCGCTGCTCTCAAT	874	
369	Db	TGTCAT	TGACTCGGTGATCTGTAGTCTCTGCTGATCCATTTTGGAGCGCTGCTTCAAT	428	
875	QY	TGCAGT	GGACAGTACTTTACTACTTTTATGCCCTCCAGTACCATAAACATCATGACGT	934	
429	Db	TGCAGT	GGACAGTACTTTACTACTTTTATGCTCTCCAGTACCATAAACATTTACAGT	488	
935	QY	GAGCGG	GTTGGATCATCATCAGATTGCATCTCGGGCGGCTTGCACGGTGTACAGCATCTT	994	
489	Db	TAA	CGGGTGGGATCAGCATAAATTTGATCTGGGAGCTTGCACGGTTTCAGGCATTTT	548	
995	QY	GTTCAT	CATTTACTCGGACAGTACTGCTGTCACTCTGCCTCATCACCATGTTCTTCAC	1054	
549	Db	GTTCAT	CATTTACTCAGATAGTAGTCTGTCACTGCCTCATCACCAGTCTTCAC	608	
1055	QY	CATGCT	GGCCCTCATGCTCTCTACGTCCACATGTTCCCTCATGCCAGAGTGCACAT	1114	
609	Db	CATGCT	GGCTCTCATGGCTTCTCTATGTCCACATGTTCTTGATGCCAGGCTTCACAT	668	
1115	QY	CAAGAG	AATGCGGCTCTCCGGGACCGGCACCATCCGGCAAGGGGCCACATGAAGGG	1174	
669	Db	TAA	GAGGATGTGTCTCTCCGGGCACTGGTGCATCCCGCAAGGTGCCAATATGAAGGG	728	
1175	QY	TGCCAT	TACCTTGACCATACTCATTTGGGTCTTCTGCTGCTGCTGGGCTCCATTTCTCCT	1234	
729	Db	AGCGAT	TACCTTGACCATCCTGATTTGGGCTCTTTGTTGCTGCTGGGCCCATTTCTCCT	788	
1235	QY	CCACTT	GATATTCTACATCTCTTGCCCCAGAAATCCATACTGTGTGTGCTCATGTCTCA	1294	
789	Db	CCACTT	AATATTCTACATCTCTTGCTCCTCAGAAATCCATATTGTGTGTGCTCATGTCTCA	848	
1295	QY	CTTTAA	CTTGACTCTGATCATGTGTAATCCATCATCTGACCCCTCTCATTTATGC	1354	

Db	849	CTTTAACTTGTATCTCATCTGATCATGTGTAAATCAATCATCGATCCTCTGATTATGC	908
Qy	1355	ACTCCGAGAGCAAGAGCTGAGGAAAAACCTTCAAGAGAGATCATCTGTTGCTGATCCTCTGGG	1414
Db	909	ACTCCGAGTCAAGACTGAGGAAAACCTTCAAGAGAGATCATCTGTTGCTATCCCTGGG	968
Qy	1415	TGGCCCTTTGTGACTTTGCTAGCAGATACTA	1444
Db	969	AGGCCCTTTGTGACTTTGCTAGCAGATATTA	998

```

RESULT 13
US-08-870-511-11
; Sequence 11, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TREATMENT OF OBESITY
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 11
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
US-08-870-511-11

```

Query Match 41.1%; Score 815.6; DB 4; Length 999;  
Best Local Similarity 89.0%; Pred. No. 2.5e-189;  
Matches 881; Conservative 0; Mismatches 109; Indels 0

455	Qy	CACCCTTTCAGACGGAAATGCACACTTCTCCACTTCTGGAAACGCACGACCTACGGACA	514
9	Db	CTCCACCCCGCTGGGATGCACACTTCTCGACTCTGGAAACCGCAGCAGTTACAGACT	68
515	Qy	GCACGGAAACGCACACTCAGTCCCTTGGCAAAAGGCTACCCGCACGGGGATGCTACGACA	574
69	Db	GCACAGCAATGCCAGTCAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTGCTACGAGCA	128
575	Qy	ACTCTTTCGTCTCCCGGAGGTGTTTCGTGACTCTCGGGGTCTATAAGCTTTCGTGGAGAACAT	634
129	Db	ACTTTTGTCTCTCCTCGAGGTGTTGTGACTCTGGGTGTCATCAGCTTGTGGAGCAATAT	188
635	Qy	TCGTGGTGATCGTGGCAATAGCCAAAGAACAGAATCTGCAGCTACCCCATGTACTTTTCAT	694
189	Db	CTTAGTGATTTGGCAATAGCCAAAGAACAGAATCTGCATTTACCCCATGTACTTTTCAT	248
695	Qy	CTCTAGCCTGGCTGTGGCCGATATGCTGGTGAGCGTTTCCAAACGGGTTCAGAGACCATCGT	754
249	Db	CTCAGCTTGGCTGTGGCTCATATGCTGGTGAGCGTTTCAATATGATCAGAAACCAATAT	308
755	Qy	CATCACCGCTTTGAAACAGTACGGATACGGAGCGCCAGAGTTTCACGGTGAATATTGTATAA	814
309	Db	CATCACCCCTATTAAACAGTACAGATATGGATGCACAGAGTTTCACAGTGAATATTGTATAA	368
815	Qy	TGTCATTGACTCCGGTGATCTGTAGTCTCTTGTCTCGCCTCGATTTTGCAGCCCTGCTCAAT	874
369	Db	TGTCATTGACTCCGGTGATCTGTAGTCTCTTGTCTCGCCTCGATTTTGCAGCCCTGCTCAAT	428
875	Qy	TGCAGTGGACAGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACCGGT	934
429	Db	TGCAGTGGACAGTACTTTACTACTCTTCTATGCTCTCCAGTACCATAACATTTATGACACT	488
935	Qy	GAGGCCGGTGGGATCATCATCATAGTTGCATCTCTGGCGCGCTTGCACGGGTGTCAGGCATCTT	994

Db 489 TAAGCGGTTGGGATCAGCATAAGTTGATCTGGGAGCTTGACGGTTTCAGGCATTTT 548  
Qy 995 GTTCATCATTTACTCGGACAGTACTGCTGTCATCATCTGCTCATCATCACCATTGTTCTTCAC 1054  
Db 549 GTTCATCATTTACTCGGACAGTACTGCTGTCATCATCTGCTCATCATCACCATTGTTCTTCAC 608  
Qy 1055 CATGCTGGCCCTCATGGCTTCTCTCTACGTCACATCTTCTCATGGCCAGACTGTCACAT 1114  
Db 609 CATGCTGGCTTCATGGCTTCTCTCTATGTCACATGTTCTCTGATGGCCAGGCTTCACAT 668  
Qy 1115 CAGAGAAATCCGCTCTCCGGGACCGGACACATCCGCAAGGGCCCAACATGAAGG 1174  
Db 669 TAAGAGGATTGCTGCTCCCGGCACTGGTGCCATCCGCAAGGTGCCAATATGAAGG 728  
Qy 1175 TGCATTTACCTTGACCATACTCATTTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234  
Db 729 AGGATTTACCTTGACCATCTGATGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788  
Qy 1235 CCACCTGATATTTACATCTCTTGTCCCGAATFCCATACTGTGTGTGTGTGTGTGTGTGTGTGT 1294  
Db 789 CCACCTAATTTACATCTCTTGTCTCTCAGAAATCCATATTTGTGTGTGTGTGTGTGTGTGTGT 848  
Qy 1295 CTTTAACCTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1354  
Db 849 CTTTAACCTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 908  
Qy 1355 ACTCCGGAGCAAGAGCTGAGGAAACCTTCAAGAGATCATCTGTTGCTATCTCTCTGCGG 1414  
Db 909 ACTCCGGAGCAAGAGCTGAGGAAACCTTCAAGAGATCATCTGTTGCTATCTCTCTGCGG 968  
Qy 1415 TGGCCTTTGTGACTTGTCTAGCAGATACTA 1444  
Db 969 AGGCTTTGTGACTTGTCTAGCAGATATTA 998

RESULT 14

US-08-671-525B-9  
; Sequence 9, Application US/08671525B  
; Patent No. 5703220  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Tadataka  
; TITLE OF INVENTION: Gantz, Ira  
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/671,525B  
; FILING DATE: June 27, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-000853DVB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810)641-1600  
; TELEFAX: (810)641-0270  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 975 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double

TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1...975  
US-08-671-525B-9  
  
Query Match 21.5%; Score 426.2; DB 1; Length 975;  
Best Local Similarity 68.6%; Pred. No. 1.6e-94;  
Matches 603; Conservative 0; Mismatches 273; Indels 3; Gaps 1;  
  
Qy 566 CTAGAGCAACTCTTCCTCTCCCGGAGGTTGTCGTGACTCTGGGGGTTCATAAGCTTGCT 625  
Db 96 CTGGAAGAATGGGCATGGCGTGGAGGTGTTCTGACCTGGGTCTCGTCAGCCCTCTT 155  
Qy 626 GGAGAACATTTCTGTGTGATCTGGCAATAGCAAGCAAGAAATCTGCACTCACCACATGTA 685  
Db 156 AGAGAACATCTGTGTGATTTGGGCGCATAGTAAAGAACAAACCTGCACTCACCACATGTA 215  
Qy 686 CTTTCTTCTGTAGCTGCTGTGGCGATATGCTGTGTGAGCTGTTCCAAAGGTCAGTA 745  
Db 216 CTTCTATGTGGGAGCTTAGCCGTGGCGACATGCTGTGTGAGCATGTCCAATGCTGGGA 275  
Qy 746 GACCATCGTCATCACCCTGTTGAACAGTACGGATACGG---ACGGCGAGATTTTCACGGT 802  
Db 276 GACTGTCCACCATATACCTTGTAAATATAAACACCTGGTATAGCCGACACCTTTGTGCG 335  
Qy 803 GAATATTGATAATGTCTGACTCGGTGATCTGTAGCTTCTGTGCTCGGCTCGATTTGCGAG 862  
Db 336 ACATCGACAAACGTGTGACTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 395  
Qy 863 CTTGCTCTCAATTGCACTGGACAGGTACTTTTACTATCTTTTATGCCCTTCCAGTACCATA 922  
Db 396 TTTGCTGGCCATTGCGTGGACAGGTACATCAACCATCTTCTATGCTTGGCTGCGCTACCACA 455  
Qy 923 CATCATCAGCGTGGGCGGTTGGGATCATCATCATGATGATGATGATGATGATGATGATGATGAT 982  
Db 456 CATCATCAGCGGAGCGGCTCGGGGTTGATCGCTGATCGCTGATCGCTTCTGATCAATAG 515  
Qy 983 GTGAGGATCTTGTTCATCATCTTACTCGGACAGTACTGCTGCTCATCATCTGCTGCTCATC 1042  
Db 516 CTGGCGCATTTGTTTCATCATCTACTATGATGATGATGATGATGATGATGATGATGATGATG 575  
Qy 1043 CATGTTCTTCAACATGCTGGCCCTCATGGCTTCTCTCTAGCTCCACATGTTTCTCATGCG 1102  
Db 576 CATGTTCTTCAACATGCTGTTCTTCTGATGTTGTTCTGTTATATACATGTTTCTCTCTG 635  
Qy 1103 CAGACTGCACATCAAGAGATCGGCTCTCCCGGACCGGACCATCCGCGAAGGGG 1162  
Db 636 CCGGAACCATGTCAAGCGGATAGCAGCTTCCCCAGATACAACTCCGTGAGGAAAGGAC 695  
Qy 1163 CAACATGAAGGTGCCATTTACCTTGACCATACTCATTTGGGGTCTTCTGCTGCTGCTGCGG 1222  
Db 696 CAGCATGAAGGGGCTATTACCCCTCACCATGCTACTGGGATTTTTCATTTGCTGCTGCTG 755  
Qy 1223 TCCATTTCTCCTCCACTTGATATTTCTACATCTTGTGTCGCCAGAAATCCATATGTTGTG 1282  
Db 756 TCCCTTCTTCTTCACTTATCTTAAATGATCTCTCCCTCCAGAACGCTTACTGCTCTTG 815  
Qy 1283 CTTTCATGCTCACATTTTAACTTTGACCTCATCTGATCATGTTGTAACCTCATCATCGACCC 1342  
Db 816 CTTTATGCTTACTTCAACATGTACCTTATCTATCTATCTATCTATCTATCTATCTATCTATCT 875  
Qy 1343 TCTCATTTATGCACTCCGAGCGCAAGAGCTGAGAAACCTTCAAGAGATCATCTGTTG 1402  
Db 876 TCTCATCTAGCCCTCCGAGCGCAAGAGATGCGGAGGACCTTTAAGGAGATCGTCTGTTG 935  
Qy 1403 CTATCTCTGCTGGTGGCCTTTGCTGACTTGTCTAGCAGATA 1441

336	ACACATCGACAAAGTGTTCGACTCCATGATCTGCATCTGTGGTGGCCCTCGATGTGCAG	395
863	CTGTCTCTCAATTGCAGTGGACAGGTACTTTTATCTATCTTTTATGCCCTCCAGTACCATAA	922
396	TTTGTGGCCATTGGGTGGACAGGTACATCACCATCTTCTATGTTCCTTGGCTTACCACCA	455
923	CATCATGACGGTGAAGCGGGTTGGATCATCATCAGTTGCATCTGGCGGCTTTCACGGT	982
456	CATCATGACGGAGGCGCTCGGGGGTGATCATCGCCTGCATCTGGACCTTCTGCATAAG	515
983	GTCAGGCATCTTGTTCATCATTTACTCGGACAGTACTGCTGTGCATCATCTGCCTCATCAC	1041
516	CTCGGGCATTTGTTTCATCATCTACTATGACTGACCAAGTATGTGATCATTTGGCCTCATCTC	575
1043	CATGTTCTTCACATGCTGGCCCTCATGGCTTCTCTCTACGTCCACATGTTCTCTCATGGC	1101
576	CATGTTCTTCACCATGCTGTTCCTCATGGTGTCTCTGTATATACACATGTTCTCTCTGGC	635
1103	CAGACTGCACATCAAGAGAATCGCCGTCTCTCCGGGACCCGGACACCATCGCCGAAGGGG	1161
636	CGGGAACCATGTCAAGCGGATAGCAGGCTTCCCCAGATACAACCTCGGTAGGCAAAAGGAC	695
1163	CAACATGAAGGTCACCTTACCTTGACCATACTCATTTGGGGTCTTCTGCTGCTGCTGGGC	1221
696	CAGCATGAAGGGGGCTATTACCTCCACCATGCTACTGGGGATTTTCATGCTGCTGGTGC	755
1223	TCCATTCCTCCACTTGATATTCTACATCTCTTGTCGCCAGAAATCCATACTGTGTGTG	1281
756	TCCCTTCTTCTTCCACCTTATCTTAATGATCTCTCTGCCCCTCAGAACGCTCTACTGCTTG	815
1283	CTTCATGCTCACTTTAACTTGTACCTTCATCTGTGATCATGTGTAACTCCATCATCGACCC	1341
816	CTTTATGTCTTACTTCAACATGTACCTTATCTACTCATCATGTGCAACTCCGATCGATCC	875
1343	TCTCTATTATGCACTCCGGAGCCAAAGAGCTGAGGAAAACCTTCAAGAGATCATCTGTGTG	1401
876	TCTCATCTACGCCCTCCGACGCCAAGAGATCGGAGGACCTTTAAGAGAGATGCTCTGTTG	935
1403	CTATCCTCTGGGTGGCCCTTTGTGACTTGTCTAGCAGATA	1441
936	TCACGGATTCGGGGACCTCTTAGGCTTCTTGGCGGGTA	974

Search completed: June 14, 2003, 10:34:02  
Job time : 89 secs

Query Match	21.5%	Score 426.2	DB 1	Length 975
Best Local Similarity	68.6%	Pred. No. 1.6e-94		
Matches 603	Conservative 0	Mismatches 273	Indels 3	Gaps 1
QY	566	CTACGAGCAACTCTTCGTCTCCCCGGAGGTTTCGTGACTCTGGGGGTCATAAGCTTGCT	625	
Db	96	CTGTGAAGAATGGGCATTCCTGTGGAGGTTCCTGACCCCTGGGTCTCGTCAGCCCTCTT	155	
QY	626	GGAGAACATTTCTGGTGATCTGTGCAATPAGCCAAAGAACAAATCTGCACATCACCCATGTA	685	
Db	156	AGAGAACATCCTGGTCATTTGGGGCCATAGTAAGAACAAANACCTGCACATCACCCATGTA	215	
QY	686	CTTTTTTCATCTGTAGCCTGGCTGTGGCCGATATGCTGGTGAGCGTTTCCAAACGGGTGAGA	745	
Db	216	CTTCTATGTGGGAGCATTTAGCCGTGGCCGACATGCTGGTGAGCATGTGCCAAATGCGTGGGA	275	
QY	746	GACCATTCGTCATCACCCCTGTTGAACAGTAGTCGGATACGG---ACGCGCAGAGTTTCACGGT	802	
Db	276	GACTGTACCCATATATCTGCTAAATATAAACACCTGGTGATAGCCGACACCTTTTGTGGC	335	
QY	803	GAATATGTGATATGTCATTGACTCGGTGATCTTAGCTTCGTCGCCCTCGAATTTTCGAG	862	



## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1985	100.0	1985	24	DNA encoding canin
2	1165.6	58.7	1708	24	DNA encoding feli
3	958.2	48.3	1671	24	Human melanocortin
4	957.8	48.3	1671	24	Human melanocortin
5	939	47.3	1671	19	Human melanocortin
6	939	47.3	1671	20	Human melanocortin
7	818.8	41.2	999	22	Nucleotide sequenc
8	817.6	41.2	1030	21	Rhesus monkey mela
9	817.4	41.2	996	18	Melanocortin-4 rec

## ALIGNMENTS

XX  
26-TTN-2000-2000MS-213909P

XX (PFIZ ) PFIZER PROD INC.  
XX Hickman MA, Houseknecht KL, Robertson AS;  
XX WPI; 2002-156598/21.  
DR P-PSDB; AAU76428.  
XX  
XX Novel canine or feline melanocortin 4 receptor polypeptide for  
PT screening modulator compounds useful for treating cachexia, anorexia,  
PT diabetes and cancer  
XX  
XX Claim 9; Fig 2; 73pp; English.  
XX  
XX The invention describes a substantially pure canine or feline  
CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be  
CC used in the treatment of appetite-related or metabolic disorders  
CC including cachexia, anorexia or weaning-induced inappetence and growth  
CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,  
CC fever, hepatic lipidosis, infection or inflammation, in a post partum  
CC sow, dairy cow, companion animal, livestock animal, poultry animal,  
CC animal suffering from shipping or crowding stress, lactating animal,  
CC obese animal or a gravid animal. (I) is useful in the generation of  
CC antibodies, as reagents in diagnostic assays, identification of other  
CC cellular gene products involved in the regulation of appetite in animals,  
CC as reagents in assays for screening for compounds that can be used in the  
CC treatment of appetite disorders in animals. A ligand of MC4R is useful  
CC for elaborating the biological function of MC4R gene product and for  
CC ameliorating appetite disorders and metabolic disorders, in animals. This  
CC sequence encodes the canine melanocortin 4 receptor (MC4R), a G-protein  
CC coupled receptor described in the method of the invention.  
XX  
XX Sequence 1985 BP; 547 A; 469 C; 456 G; 513 T; 0 other;  
SQ

Query Match 100.0%; Score 1985; DB 24; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAAGACCGTGGGAGGAGCTGATGCGAATGTGACGAGATTTCAGCTCCTGGTGGC 60  
DB 1 CTAAGACCGTGGGAGGAGCTGATGCGAATGTGACGAGATTTCAGCTCCTGGTGGC 60  
QY 61 TGGGGCGAATCGGAGGAGTACTTGGCAACAGCTCCTGAAATGCCCTAGACTAAAGTT 120  
DB 61 TGGGGCGAATCGGAGGAGTACTTGGCAACAGCTCCTGAAATGCCCTAGACTAAAGTT 120  
QY 121 RAGTGGGAGTGGAGACAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 180  
DB 121 RAGTGGGAGTGGAGACAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 180  
QY 181 AAAAAAGAAAGAGAGAGCTTTGAATGAATGAGCATTTTCAGAAATCGAAGATGTTA 240  
DB 181 AAAAAAGAAAGAGAGAGCTTTGAATGAATGAGCATTTTCAGAAATCGAAGATGTTA 240  
QY 241 CAGTGAAGGTGATCGGAGCTGTACCTGGAAGACAGTAAGAGCTCCACTGCCAGCCTTTG 300  
DB 241 CAGTGAAGGTGATCGGAGCTGTACCTGGAAGACAGTAAGAGCTCCACTGCCAGCCTTTG 300  
QY 301 GAGCAGGAGAGAGTACTCAACACCTGGCAGGCCAGCTGGATCCTCAGAACTTTGGGAGC 360  
DB 301 GAGCAGGAGAGAGTACTCAACACCTGGCAGGCCAGCTGGATCCTCAGAACTTTGGGAGC 360  
QY 361 CACGAGAGGGGAGAAACATCACCGGGCTCCCTGGCTGGAGAGGCCGAATCAGTCCCGA 420  
DB 361 CACGAGAGGGGAGAAACATCACCGGGCTCCCTGGCTGGAGAGGCCGAATCAGTCCCGA 420  
QY 421 GGGGGTCTGCATACACTTGTGTCAGGATGAATCCACCTTTGAGCAGCGGAATGACACTT 480  
DB 421 GGGGGTCTGCATACACTTGTGTCAGGATGAATCCACCTTTGAGCAGCGGAATGACACTT 480  
QY 481 CTCCTCACTTCTGGAAACCGAGCAGCTACGAGACAGCAGCGGCAACCGCACTGAGTCCCTTG 540  
DB 481 CTCCTCACTTCTGGAAACCGAGCAGCTACGAGACAGCAGCGGCAACCGCACTGAGTCCCTTG 540

QY 541 GCAAAAGGCTACCCCGACCGGGGATGCTACGAGCAACTCTTCTGCTCTCCCGAGGTTGCG 600  
DB 541 GCAAAAGGCTACCCCGACCGGGGATGCTACGAGCAACTCTTCTGCTCTCCCGAGGTTGCG 600  
QY 601 TGACTCTGGGGTCAATAAGCTTGTGGAGAACATTTCTGGTGATCGTGGCAATAGCAAGA 660  
DB 601 TGACTCTGGGGTCAATAAGCTTGTGGAGAACATTTCTGGTGATCGTGGCAATAGCAAGA 660  
QY 661 ACAAGAACTGCACTACCCCATGTAATTTTTCATCTGTAGCTGCTGGCCGATATGC 720  
DB 661 ACAAGAACTGCACTACCCCATGTAATTTTTCATCTGTAGCTGCTGGCCGATATGC 720  
QY 721 TGGTGAGGCTTCCAAACGGGTGAGAGACATCGTCATCACCTGTTGAACAGTACGGATA 780  
DB 721 TGGTGAGGCTTCCAAACGGGTGAGAGACATCGTCATCACCTGTTGAACAGTACGGATA 780  
QY 781 CGGACGCGCAGAGTTTTCACGGTGAATATGTAATGTGATGATGATGATGATGATGATGAT 840  
DB 781 CGGACGCGCAGAGTTTTCACGGTGAATATGTAATGTGATGATGATGATGATGATGATGAT 840  
QY 841 CTTGCTCGCTCGATTTGACGGCTGCTCAATTTGCAAGTGGAGAGTACCTTACTATCT 900  
DB 841 CTTGCTCGCTCGATTTGACGGCTGCTCAATTTGCAAGTGGAGAGTACCTTACTATCT 900  
QY 901 TTTATGCCCTCCAGTACCATTAACATCATGAGCGGTGAGCGGTGGGATCATCATCATCT 960  
DB 901 TTTATGCCCTCCAGTACCATTAACATCATGAGCGGTGAGCGGTGGGATCATCATCATCT 960  
QY 961 GCATCTGGGGCGCTTGGACGGTGTGACGATCTTGTTCATCATTTACTTGGACAGTACTG 1020  
DB 961 GCATCTGGGGCGCTTGGACGGTGTGACGATCTTGTTCATCATTTACTTGGACAGTACTG 1020  
QY 1021 CTGTCATCATCTGCTCATCACCATTCTTTCACCATGCTGGCCCTCATGCTCTCTCT 1080  
DB 1021 CTGTCATCATCTGCTCATCACCATTCTTTCACCATGCTGGCCCTCATGCTCTCTCTCT 1080  
QY 1081 ACGTCCACATGTTCTCATGCGGAGCTGCATCAAGAGAAATCGCCCTCTCCCGGGCA 1140  
DB 1081 ACGTCCACATGTTCTCATGCGGAGCTGCATCAAGAGAAATCGCCCTCTCCCGGGCA 1140  
QY 1141 CCGGACCATCTCCGCAAGGGGCCAATGAGAGGTGCCATTTACTTGGACATCATCATCTG 1200  
DB 1141 CCGGACCATCTCCGCAAGGGGCCAATGAGAGGTGCCATTTACTTGGACATCATCATCTG 1200  
QY 1201 GGGTCTTCTGCTGCTGGGCTCCATTTCTCCCTCCACTTGATATTTACATCTCTGTC 1260  
DB 1201 GGGTCTTCTGCTGCTGGGCTCCATTTCTCCCTCCACTTGATATTTACATCTCTGTC 1260  
QY 1261 CCCAGAAATCCATCTGCTGCTCATCTCTCATCTTTAACTTTGACCTCATCTCTGATCA 1320  
DB 1261 CCCAGAAATCCATCTGCTGCTCATCTCTCATCTTTAACTTTGACCTCATCTCTGATCA 1320  
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DB 1321 TGTGTAATCCATCATGACCCCTCTCATTTATGCACTCCGAGGCCAAGAGCTGAGGAAA 1380  
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DB 1381 CTTTCAAGAGATCATCTGTTGCTATCTCTGGGTGGCTTTGTGACTTGTCTAGCAGAT 1440  
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DB 1441 ACTAGCTGGGACAGAGGAAGTACTAAAAACATGCACACAGAGACTTCTTCTCTCAC 1500  
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QY 734 CAACGGGTACAGACCATCGTCATCACCCCTGTTGAACAGTACGATACGACGACGAG 793
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DB 798 TTTCAGGTGAATATTGATTAATGTCATGACTCGGTGATGTCGTGCTTCGCTC 857
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DB 858 GATTTCAGGCTGCTCCTCAATTCAGTGGACAGGTACTTACTATCTTTATGCCCCCA 917
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QY 974 TTGCAGGTGTCAGGATCTTTTCATCATTTACTCGGACAGTACGTCGTGTCATCAT 1033
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DB 1218 CTGCTGGGTCCATCTCTCCACATGATATCTACATCTCTGTCGCCAGAAATCCATA 1277
QY 1274 CTGCTGGGTCCATCTCTCCACATGATATCTACATCTCTGTCGCCAGAAATCCATA 1333
DB 1278 CTGCTGGGTCCATCTCTCCACATGATATCTACATCTCTGTCGCCAGAAATCCATA 1337
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DB 1338 CATCGACCTCTCATTTATGCACTCCGAGCCAGAGCTGAGAGAAACCTTCAAGAGAT 1397
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DB 1398 CATCTGTTGCTATCTCTGGGTGGCTTTGTCATGTCATGTCATGTCATGTCGAG 1457
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DB 1568 ATTAAGTTACATGACTTTTGTGNAATGGAACATGCCAGTCTCTGATCACTTAA 1627
QY 1634 TGTCATGCTATTTTGGGTGTCATGTTGTAATCCAT-TTCGACGCTGTGACACATTTGA 1692
DB 1628 TGCTTGTCTACTTTTGGGTGTACAAATGTAATCCATATATAGTGTGTGAGCACTATGA 1687
QY 1693 ATTTCTAGAAAAA 1711
DB 1688 ATGTATAAAAAA 1706
```

RESULT 3

AAD25896

ID AAD25896 standard; DNA; 1671 BP.

```
XX AAD25896;
XX AC
XX DT
XX DE
XX DE Human melanocortin 4-receptor (MC4R) gene #1.
XX KW Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
XX KW MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
XX KW ASO; gene therapy; anorectic; chromosome 18q22; ds.
XX OS Homo sapiens.
XX FH Key
XX FH Location/Qualifiers
XX FH replace (216, C)
XX FT /tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT /note= "Polymorphic site (PS) 1"
XX FT exon 394..1392
XX FT /tag= b
XX FT /number= 1
XX FT CDS 394..1392
XX FT /tag= c
XX FT /product= "Human melanocortin 4-receptor (MC4R)"
XX FT variation replace (700, G)
XX FT /tag= d
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT /note= "Polymorphic site (PS) 2"
XX FT variation replace (920, T)
XX FT /tag= e
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT /note= "Polymorphic site (PS) 3"
XX FT variation replace (987, T)
XX FT /tag= f
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT /note= "Polymorphic site (PS) 4"
XX FT variation replace (999, A)
XX FT /tag= g
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT /note= "Polymorphic site (PS) 5"
XX FT variation replace (1144, C)
XX FT /tag= h
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT /note= "Polymorphic site (PS) 6"
XX WO200179222-A2.
XX PN
XX PD 25-OCT-2001.
XX PF 12-APR-2001; 2001WO-US111943.
XX PR 12-APR-2000; 2000US-196677P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Bentivegnà SC, Choi JY, Kazemi A, Lee HH, Nandabalan K, Parks KE;
XX PI Sausker EA;
XX WPI: 2002-082744/11.
XX P-PSDB; AAE15746.
XX Novel polymorphic variants of melanocortin 4-receptor gene useful in
XX studying expression and function of the protein, useful for screening
XX candidate drugs to treat diseases related to the protein activity e.g.
XX obesity
XX Claim 19; Fig 1; 53pp; English.
XX The invention relates to single nucleotide polymorphisms (SNP) in human
XX melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful
XX for improving the efficiency and reliability of several steps in the
XX discovery and development of drugs for treating diseases associated
XX with MC4R activity, e.g. obesity. MC4R gene is useful in studying the
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Db 448 AGCAGTTACAGACTGCACAGCAATGCCAGTCCCTTGGAAAAGGCTACTCTGATGGA 507  
QY 561 GGATGCTACGAGCAACTCTCTGCTCCCGGAGGTTGTCGACTCTGGGGTGCATAGC 620  
Db 508 GGGTCTACGCGCAACTTTTGTCTCTCTGAGGTGTTGACTCTGGGTGATCAGC 567  
QY 621 TTGCTGGAGAACATTTCTGGTGTGTCGCAATAGCCAAAGAACAAATCTGCATCCACC 680  
Db 568 TTGTTGGAGAAATCTTAGAGATTGTGCAATAGCCAAAGAACAAATCTGCATCCACC 627  
QY 681 ATGTACTTTTTCATCTGTAGCTGGCTGGTGGCCGATATGCTGGTGGAGGTTTCCAAACGGG 740  
Db 528 ATGTACTTTTTCATCTGCAGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 687  
QY 741 TCAGAGCAATCGTCATCACCTGTGACAGTACGATACGAGCGCCAGAGTTTCAG 800  
Db 588 TCAGAACCAATATCATCACCTATTAACCGTACAGATACGAGTGCACAGATTTCACA 747  
QY 801 GTGAATATTGATAATGTCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 860  
Db 748 GTGAATATTGATAATGTCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807  
QY 861 AGCCTGCTCTCAATGTGAGTGGAGGACTTTTACTATTTTATGCGCTCCAGTACCAT 920  
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QY 921 AACATCATGAGGTTGAGGCGGTTGGGATCATCATCATCATCATCATCATCATCATCATCAT 980  
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QY 981 GTGCAGGCACTTTGTTTCATCATTTACTTCGACAGTACTGTGTCTCATCATCATCTGCTCATC 1040  
Db 928 GTTTCAGGCACTTTGTTTCATCATTTACTTCAGATAGTAGTGTGTCTCATCATCTGCTCATC 987  
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QY 1101 GCCAGACTGCACATCAAGAGAAATCGCGTCTCCCGGCGACCGCCACCATCCGCCAGGG 1160  
Db 1048 GCCAGGCTTCACATTAAGAGGATGTGCTCTCTCCCGGCGACTGGTGCCATCCGCCAAGGT 1107  
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Db 1108 GCCAATATGAAGGAGCGATTAACCTTGACCACTACTCAATTTGGGGTCTTCTGCTGCTGG 1167  
QY 1221 GCTCATCTTCTCTCCACTTGATATTTACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1280  
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QY 1281 TGCTTCATGCTCACTTTAACTTGTACTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1340  
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QY 1341 CCTCTCAATTTATGCACTCCGGAGCAAGAGTGGAGAAACCTTCAAGAGATCATCTGT 1400  
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QY 1401 TGCTATCTCTGGTGGCTTTGTGACTTGTCTAGCAGATACTAGTGGGACAGAGAA 1460  
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QY 1461 GTACTAAA--AACATGACCAGAGACTTCTTCATCTCCACACACATGAATCTGTGCTT 1518  
Db 1408 GCAATATAGGAACATCCATAAGAGACTTTTTCAGTCTTACCTCTTACCTCTTACCTCTTACCT 1467  
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QY 1579 ACTTTATGATGTTTGTGTAAGAAAAAATGCCAGGCTCTGTA-CATTGCTAAATGTC 1637  
Db 1527 AGCCTATGATTTTT- - - - -AATGAGAAAAAATGCCAGTCTCTGTATTTTCCAAATCTC 1581

QY 1638 ATGCTAC-TTTTGGCTGTGCATTTAATCCAT-TTCGAGCTGTAGACACTTTGAATT 1695  
Db 1582 ATGCTACTTTTGGCCATAAATATGAATCTATGTTATAGTTGTAGGCACTCTGGATT 1641  
QY 1696 TCTAGAAAGAAA 1708  
Db 1642 TACAAAAGAAAA 1654  
RESULT 7  
AAF85465  
ID AAF85465 standard; DNA; 999 BP.  
XX AAF85465;  
AC AAF85465;  
XX  
DT 23-JUL-2001 (first entry)  
XX Nucleotide sequence of a human melanocortin-4 receptor (MC-R4).  
DE Human; melanocortin-4 receptor; MC-R4; transgenic animal; body weight;  
KW food intake; obesity; diabetes; anorexia; cachexia; cancer;  
KW sexual dysfunction; pain; impaired memory; neuronal regeneration;  
KW neuropathy; growth disorder; growth hormone;  
KW insulin-like growth factor-1; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..999  
FT /\*tag= a  
FT /product= "melanocortin-4 receptor (MC-R4)"  
XX  
PN WO200133956-A1.  
XX  
PD 17-MAY-2001.  
XX  
PF 13-NOV-2000; 2000WO-US31061.  
XX  
PR 12-NOV-1999; 99US-0165074.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Van Der Ploeg LPT, Chen AS, Chen HV, Forrest MJ, MacIntyre DE;  
PI Metzger JM, Palyha OC, Feighner SD, Hreniuk D;  
XX  
DR WPI; 2001-343541/36.  
DR P-PSDB; AAB68490.  
XX  
PT New transgenic animal with non-functional gene for melanocortin-4  
PT receptor, useful for identifying specific modulators, potentially used  
PT for treating obesity or diabetes.  
XX  
PS Disclosure; Fig 1; 58pp; English.  
XX  
CC The present sequence encodes a human melanocortin-4 receptor (MC-R4).  
CC The specification describes transgenic non-human animals whose somatic  
CC and germ cells contain at least one non-functional gene for MC-4R  
CC protein. The transgenic animals, or cells derived from them, are used  
CC to screen for compounds that modulate MC-4R. These modulators are  
CC potentially useful for regulating body weight and food intake and  
CC treatment of associated diseases, obesity; diabetes; anorexia; cachexia;  
CC cancer; sexual dysfunction; pain; impaired memory or neuronal  
CC regeneration; neuropathy; growth disorders linked to growth hormone  
CC and insulin-like growth factor-1. They can also be used to study MC-4R  
CC expression and activity.  
XX  
SQ Sequence 999 BP; 229 A; 243 C; 213 G; 314 T; 0 other;

Query Match 41.2%; Score 818.8; DB 22; Length 999;  
Best Local Similarity 89.2%; Pred. NO. 4.5e-184;  
Matches 883; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

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QY 455 CACCCTTACGACGGAATGACACACTTCTCTCCACTTCTGGAACCCGACGACCTACGAGCA 514
Db 9 CTCACCCACCCGCTGGGATGACACACTTCTCTGACCTCTGGAACCCGACGAGTTACAGACT 68
QY 515 GCACGGCAGCCGACCTAGTCCCTTGGCAAGGCTACCCGAGCGGGGATGCTACGAGCA 574
Db 69 GCACAGCAATGCCAGTGAAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTGTCTACGAGCA 128
QY 575 ACTCTTCTGCTCCCGGAGGTGTCTGAGCTCTGGGGGTCAATAGCTTGTGAGAACAT 634
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QY 635 TCTGGTGAATCGGGCAATAGCAAGAACAGAAATCTGCACCTACCCCATGTACTTTTCAT 694
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QY 695 CTGTAGCCTGGCTGTGGCGGATATGCTGTGAGCGTTTCCAAAGGTCAGAGCAACATCT 754
Db 249 CTGCAGCTTGGCTGTGGCTGATATGCTGTGAGCGTTTCAAATGGATCAGAAACCATAT 308
QY 755 CATCACCTTGTGAACAGTACGATACGGACGCGAGAGTTTCACGGTGAATATTGATAA 814
Db 309 CATCACCTTATAACAGTACAGATACGATACGAGAGTTTCACAGTGAATATTGATAA 368
QY 815 TGTCAATGACTCGGTGATCTGAGTCCCTTGTCTGCGCTCGATTTGAGCCTGCTCTCAAT 874
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QY 875 TGCAGTGGACAGTACTTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGT 934
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QY 935 GAGCGGGTGGGATCATCATGATGTCATCTGGGGGCTTGCAGGGTGTGACAGGATCTT 994
Db 489 TAAGCGGTGGGATCATCATGATGTCATCTGGGGGCTTGCAGGGTGTGACAGGATCTT 548
QY 995 GTTCATCATTTACTCGGACAGTACTGCTGTATCATCTGCTCATCACCATGTTCTTAC 1054
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Db 609 CATGTGGCTCATGCTTCTCTATGTCACATGTTCCCTCATGGCCAGGCTTCACAT 668
QY 1115 CAAGAAATCGCGCTCTCCCGGACCGGACCATCCGCCAAGGGGCCAATCAAGAGG 1174
Db 669 TAAGAGGATGCTGCTCCCGGACCTGGTGCCATCGCCAAAGTGCCAAATATGAAGG 728
QY 1175 TGCATTAATGACCATCAATTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
Db 729 AGCGATTACCTTGACCATCTGATTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 788
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Db 969 AGGCCTTTGTGACTTGTCTAGCAGATACTA 998
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RESULT 8  
AAA26972  
ID  
XX

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AAA26972;
04-AUG-2000 (first entry)
Rhesus monkey melanocortin-4 receptor gene.
Rhesus monkey; rhodopsin; G-protein coupled receptor; anorectic;
melanocyte stimulating hormone; melanocortin receptor; obesity; ss.
Macaca mulatta.
Key Location/Qualifiers
CDS 17..1015
FT /tag= a
FT /product= "melanocortin-4 receptor protein"
XX WO200027863-A1.
XX 18-MAY-2000.
XX 05-NOV-1999; 99WO-US25767.
XX 09-NOV-1998; 98US-0107721.
XX (MERI ) MERCK & CO INC.
XX MacNeil DJ, Weinberg DH, Van Der Ploeg LHT;
XX WPI: 2000-376480/32.
XX P-PSDB; AAY94301.
XX Novel DNA encoding rhesus monkey melanocortin 4 receptor protein,
recombinant vectors and host cells, useful in methods for identifying
selective agonists and antagonists
XX Claim 1: Page 35; 53pp; English.
XX The present sequence encodes the rhesus monkey melanocortin-4
receptor protein (MC-4R). Melanocortin receptors belong to the
rhodopsin sub-family of G-protein coupled receptors. They bind and are
activated by peptides such as alpha-, beta-, or gamma-melanocyte
stimulating hormones derived from the pro-opiomelanocortin gene and they
are believed to mediate a wide range of physiological functions.
XX The rhesus MC-4R gene was isolated by PCR using a series of four
oligonucleotides (AAA26973-A26976) based on the human MC-4R gene sequence
and designed to incorporate a restriction enzyme site for cloning into
the expression vector pCI-neo. The recombinant vector was transfected
into DH5a cells in preparation for DNA sequencing. The present sequence
or a mutated form may be introduced into an expression vector for
expression in host cells. The subcellular membrane fractions will
comprise either wild-type or mutant forms of rhesus MC-4R at enhanced
levels and can be used in assays to identify ligand binding, activators
and modulators, agonists and antagonists of MC-4R. This will allow for
selection of compounds that are active for the rhesus receptor in vitro
and will allow the selection of novel drugs to treat obesity.
XX SQ Sequence 1030 BP; 239 A; 254 C; 222 G; 315 T; 0 other;
Query Match 41.2%; Score 817.6; DB 21; Length 1030;
Best Local Similarity 87.4%; Pred. No. 8.8e-184;
Matches 895; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 436 CTTGTTGAGGATGAACATCCACCTTTCAGACGGAATGCACACTTCTCTCCACTTCTGGA 495
Db 6 CTCCTGCCAGCATGTTGAATCCACCTCCACCTGGGATGTCACGCTTCTCTGCACCTCTGGA 65
QY 496 ACCGAGCACTACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 555
Db 66 ACCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 125
QY 556 ACGGGGATGTACGAGCAACTTTCGTCCTCCCGGAGGTGTCGTGACTCTGGGGTCA 615
Db 126 ATGGAGGTGCTACGAGCAACTTTTGTGTCCTCTCTCTGAGGTGTTGTGACTGCTGGTGTC 185
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Oy 616 TAAGCTTGTCTGGAGAACATTTCTGTGATCTGTCGCAATAGCCAAAGAACAAAGAAATCTGCAC 675
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Db 186 TCAGCTTGTGGAGAAATATCTAGTGTGTCGCAATAGCCAAAGAACAAAGAAATCTGCAT 245
Oy 676 CACCCATGTACTTTTTCATCTGTAGCTGGCTGGCGGATATGCTGTGAGCGTTTCCA 735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 CACCCATGTACTTTTTCATCTGCAGCTGGCTGGCTGTGATATGCTGTGAGCGTTTCAA 305
Oy 736 ACAGGTGACAGACCATCGTATCACCTGTTGAACAGTACGATACGACGCGAGAGTT 795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 ATGGATCAGAACCATTGTCTATCACCTATTAAACAGTACGATACGACACAGAGTT 365
Oy 796 TCACGGTGAATTAATGATAATGATCTGCTGCTGATCTGTAGTCTCTGCTGCCCTCGA 855
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Db 366 TCACAGTGAACATTTGATAATGTTATGACTCAGTGATCTGTAGTCTCTGCTGCCATCA 425
Oy 856 TTTGACGCTGCTCTCAATGCACTGGACAGGTAATTTACTATCTTTTATGCCCTCCAGT 915
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 TTTGACGCTGCTTTCAATGCACTGGACAGGTAATTTACTATCTTTTATGCCCTCCAGT 485
Oy 916 ACCATAACATCATGACGGTGGCGGTTGGGATCATCATCAGTTGCTATGCTGGCGGCTT 975
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Db 486 ACCATAACATCATGACGGTGGCGGTTGGGATCATCATCAGTTGCTATGCTGGCGGCTT 545
Oy 976 GCACGGTGTACAGGATCTTGTTCATCAATTTACTCGGACAGTACTGCTGTCATCTGCC 1035
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 546 GCACGGTGTACAGGATCTTGTTCATCAATTTACTCGGACAGTACTGCTGTCATCTGCC 605
Oy 1036 TCATCAGATGTTCTTCCACATGCTGGCCCTCATGCTGCTCTCTAGTCCACATGTTCC 1095
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 606 TCATCAGATGTTCTTCCACATGCTGGCCCTCATGCTGCTCTCTAGTCCACATGTTCC 665
Oy 1096 TCATGGCCAGACTGCATCAAGAGATCGCGCTCTCCCGGACCGGACCATCCGCC 1155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 666 TGATGGCCAGGCTTCACATTAAGAGGATGCTGCTCCCGGACCGGACCATCCGCC 725
Oy 1156 AAGGGCCCAACATGAAGGGTGCCTTACCTTGACCATCTCATTTGGGCTCTTCTGCTCT 1215
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 726 AAGGGCCCAATGAAGGGAGCGATTACTTTGACCATCTCTGATTTGGGCTCTTCTGCTCT 785
Oy 1216 GCTGGGCTCATCTTCTTCCATGATATTTCTACATCTCTTGTCCCGAGAAATCCACT 1275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 786 GCTGGGCCCCATTTCTTCCACATTAATTTCTACATCTCTTGTCCCTCAGAATCCATTT 845
Oy 1276 GTGTGTGCTGCTCATCTCAGTTTAACTGTACCTCATCTGATGTAATCCATCA 1335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 846 GTGTGTGCTGCTCATCTCAGTTTAACTGTACCTCATCTGATGTAATCCATCA 905
Oy 1336 TCGACCTCTCATTTATGCACTCCGGAGCCAAAGAGCTGAGGAAACCTTCAAAGAGATCA 1395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 906 TCGATCTCTGATTTATGCACTCCGGAGTCAAGAACTAAGGAAACCTTCAAAGAGATCA 965
Oy 1396 TCTGTGTGATATCTCTGGTGGCCCTTTGTGACTTTGTCTAGCAGATAGTCTGGGACAG 1455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 966 TCTGTGTGATATCTCTGGGAGCCCTATGTGACTTTGTCTAGCAGATATTAATGGGACAG 1025
Oy 1456 AGGA 1459
    |||
Db 1026 AGCA 1029
```

## RESULT 9

AAAT68790

ID AAAT68790 standard; DNA; 996 BP.

XX

AAAT68790;

XX

19-AUG-1997 (first entry)

XX

DE Melanocortin-4 receptor coding sequence.

XX

KW Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;



```
QY 1055 CATGCTGGCCCTCATGGCTTCTCTAGTCCACATGTTCTCATGGCCAGACTGCACAT 1114
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 609 CATGCTGGCTCTCATGGCTTCTCTATGTCACATGTTCTGATGGCCAGGCTTCAT 668
QY 1115 CAAGAGAAATCCGCTCTCCGGGACCGGACCATCGCCAAAGGGCCAAACATGAAGG 1174
||||| || || || || || || || || || || || || || || || || || || || ||
Db 669 TAAGAGGATGCTGCTCTCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATGAAGG 728
QY 1175 TGCCATTACCTTGACCATACATTTGGGGTCTTCGTGCTGCTGGGCTCCATTTCTCCT 1234
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 729 AGCATTACCTTGACCATCTGATGGGCTCTTTGTTGCTGCTGGGCCCATTTCTCCT 788
QY 1235 CCACCTTGATATTACATCTCTTGTCCCGAGAACTCCATACATGTTGCTTCATGTCCTCA 1294
||||| || || || || || || || || || || || || || || || || || || || ||
Db 789 CCACCTTAATATTACATCTCTTGTCTCAGAACCCATATTGTTGTTGCTTCATGTCCTCA 848
QY 1295 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1354
||||| || || || || || || || || || || || || || || || || || || || ||
Db 849 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 908
QY 1355 ACTCCGGAGCAAGAGCTGAGAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG 1414
||||| || || || || || || || || || || || || || || || || || || || ||
Db 909 ACTCCGGAGTCAAGAACTGAGAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG 968
QY 1415 TGGCTTTGTGACTTGTCTAGCAGATA 1441
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 969 AGGCTTTGTGACTTGTCTAGCAGATA 995

RESULT 11
AAV06400
ID AAV06400 standard; DNA; 996 BP.
XX AC AAV06400;
XX DT 30-APR-1998 (first entry)
XX DE Human melanocortin-4 (MC4) receptor encoding DNA.
XX KW Melanocortin receptor; ligand; MC4; human; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 1..996
XX FT /*tag= a
XX FT /product= melanocortin-4 receptor
XX FT /note= "stop codon is not indicated"
XX PN US5703220-A.
XX PD 30-DEC-1997.
XX PF 27-JUN-1996; 96US-0671525.
XX PR 17-FEB-1994; 94US-0200711.
XX PR 27-JUN-1996; 96US-0671525.
XX PA (UNMI ) UNIV MICHIGAN.
XX PA Gantz I, Yamada T;
XX PI WPI; 1998-076484/07.
XX DR P-PSDB; AAW33724.
XX PT DNA encoding human melanocortin-4 receptor - and cells useful in
XX PT assay for MC4 receptor ligands
XX PS Claim 7; Columns 43-46; 59pp; English.
XX CC This DNA encodes a human melanocortin receptor-4 (MC4). The MC4 receptor
XX CC of this invention is activated by amino acids in the carboxyl and amino
```

```
CC terminal portions of the heptapeptide sequence shared by all the
CC melanocortin peptides. MC4 is expressed primarily in brain and is notably
CC absent in the adrenal cortex, melanocytes and placenta. The MC4 receptor
CC gene was localised to chromosome loci 18q21.3. The invention provides
CC methods to identify ligands that bind to MC4 receptor.
XX
SQ Sequence 996 BP; 227 A; 243 C; 213 G; 313 T; 0 other;
Query Match 41.2%; Score 817.4; DB 19; Length 996;
Best Local Similarity 89.3%; Pred. No. 9.6e-184;
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 455 CACCTTTTCAGCAGCGGAATGCACACTTCTCTCCACTTCTGGAACCGCAGCACTAGCGACA 514
Db 9 CTTCCACCACCGTGGGATGCACACTTCTCTGCACCTCTGGAACCGCAGCACTTACAGACT 68
QY 515 GCACGGCAACCCCACTGAGTCCCTTGGCAAGGCTACCCCGACGGGGATGCTAGCAGCA 574
Db 69 GCACAGCAATCCCACTGAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTCTACGAGCA 128
QY 575 ACTCTTGTCTCCCGGAGGTTTTCGTGACTCTGGGGTCTATAAGCTTGTCTGGAGAATAT 634
Db 129 ACTTTTGTCTCTCTGAGGTTTTCGTGACTCTGGGGTCTATCAGCTTGTGGAGAATAT 188
QY 635 TCTGTGATCTGTCGCAATAGCAAGCAAGAACTTGCACCTCACCCATGTACTTTTTCAT 694
Db 189 CTTAGTGATTTGGCAATAGCAAGCAAGAACTTGCATTCACCCATGTACTTTTTCAT 248
QY 695 CTGTAGCCTGGCTGTGGCCGATATGCTGGTGAGGCTTTTCCACGGGTTCAGAGACCATCGT 754
Db 249 CTGCAGCTTGGCTGTGGCTGATATGCTGGTGAGGCTTTTCAAATGATCAGAAACCATTAT 308
QY 755 CATCACCTTGTGAACAGTACGAGTACGAGCGCGCAGAGTTTCACGGTGAATATTGATAA 814
Db 309 CATCACCTTATTAACAGTACAGATACGAGTTCACAGAGTTTCACAGTGAATATTGATAA 368
QY 815 TGTCAATTGACTCGGTGATCTGTAGTCTCTTCTCGCCTTCGATTTTGCACCTGCTCTCAAT 874
Db 369 TGTCAATTGACTCGGTGATCTGTAGTCTCTTCTGTCATCCATTTTGCACCTGCTTCAAT 428
QY 875 TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCCCTCCAGTACCATAACATCATGACGGT 934
Db 429 TGCAGTGGACAGGTACTTTACTATCTTCTATGCTCTCCAGTACCATAACATCATGACAGT 488
QY 935 GAGCGGTTGGGATCATCATCAGTTCATCTGGCGGCTTTCAGCGGTTCAGGCATCTT 994
Db 489 TAAGCGGTTGGGATCATCATCAGTTCATCTGGCGGCTTTCAGCGGTTCAGGCATCTT 548
QY 995 GTTCATCATTTTACTCGGACAGTACTGTCTCATCTGCTCATCTGCTCATCAGCTGTTCTTCCAC 1054
Db 549 GTTCATCATTTTACTCAGATAGTGTCTCATCTGCTCATCTGCTCATCAGCTGTTCTTCCAC 608
QY 1055 CATGCTGGCCCTCATGGCTTCTCTCTAGTCCACATGTTCTCATGGCCAGCTGCACAT 1114
Db 609 CATGCTGGCTCTCATGGCTTCTCTCTATGTCACATGTTCTGATGGCCAGGCTTCAT 668
QY 1115 CAAGAGAAATCCGCTCTCCGGGACCGGACCATCCGCCAAGGGCCAAACATGAAGG 1174
Db 669 TAAGAGGATGCTGCTCTCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATGAAGG 728
QY 1175 TGCCATTACCTTGACCATACATTTGGGGTCTTCGTGCTGCTGGGCTCCATTTCTCCT 1234
Db 729 AGCATTACCTTGACCATCTGATGGGCTCTTTGTTGCTGCTGGGCCCATTTCTCCT 788
QY 1235 CCACCTTGATATTACATCTCTTGTCCCGAGAACTCCATACATGTTGCTTCATGTCCTCA 1294
Db 789 CCACCTTAATATTACATCTCTTGTCTCAGAACCCATATTGTTGTTGCTTCATGTCCTCA 848
QY 1295 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1354
Db 849 CTTTAACTTGATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 908
QY 1355 ACTCCGGAGCAAGAGCTGAGAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG 1414
```

Db	909	ACTCCGGAGTCAAGAACTGAGGAAAACCTTCAAGAGATCATCTGTTGCTATCCCTGGG	968
QY	1415	TGGCCTTTGTGACTTGTCTAGCAGATA	1441
Db	969	AGGCCTTTGTGACTTGTCTAGCAGATA	995
RESULT 12			
AAAX01964			
ID	RAX01964 standard; DNA; 996 BP.		
XX	AAAX01964;		
XX	21-APR-1999 (first entry)		
DT	Human MC4 DNA.		
DE			
XX			
KW	Melanocortin-4 receptor; MC1; MC2; MC3; MC4; MC5; detection; probe;		
KW	receptor binding; secondary signalling; tissue distribution; ds.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..996	
FT		/*tag= a	
FT		/product= "MC4"	
FT		/note= "partial sequence, no stop codon given"	
XX	US5869257-A.		
PN	XX		
XX	09-FEB-1999.		
PD	XX		
XX	23-APR-1997;	97US-0842238.	
XX	17-FEB-1994;	94US-0200711.	
PR	27-JUN-1996;	96US-0671525.	
PR	23-APR-1997;	97US-0842238.	
XX	(UNMI ) UNIV MICHIGAN.		
PA	Gantz I, Yamada T;		
PI	WPI; 1999-152760/13.		
XX	P-PSDB; AAW92442.		
DR	Probe for detecting melanocortin-4 receptor genes - that		
XX	specifically hybridises to defined DNA sequence		
PT	Example 1; Column 43-46; 60pp; English.		
XX	This sequence encodes the human melanocortin-4 receptor, MC4. This		
XX	protein is used in a method in which a nucleic acid probe useful for		
CC	specifically detecting melanocortin-4 receptor genes is described.		
CC	This probe is used to isolate genes encoding melanocortin receptors,		
CC	to characterise melanocortin receptor binding and secondary signalling		
CC	and to determine tissue distribution of the melanocortin receptors.		
XX	Sequence 996 BP; 227 A; 243 C; 213 G; 313 T; 0 other;		
SQ			
Query Match 41.2%; Score 817.4; DB 20; Length 996;			
Best Local Similarity 89.3%; Pred. No. 9.6e-184;			
Matches 881; Conservative 0; Mismatches 106; Indels 0; Gaps 0;			
QY	455	CACCCTTCAGCAGGAATGCACACTTCTCTCCACTTCTGGAACCGCAGCACCTACGGACA	514
Db	9	CTCCACCCACCGTGGGATGCACACTTCTCTGCACCTCTGGAACCGCAGGTACAGACT	68
QY	515	GCACGGCAACGCACTGAGTCCCTTGGCAAGGCTACCCGACGGGATGCTACGAGCA	574
Db	69	GCACAGCAATGCCAGTGAAGTCCCTTGGAAAGGCTACTCTGATGAGGGTGTCTACGAGCA	128
QY	575	ACTCTTCGCTCTCCCGGAGGTGTTCTGCTGACTCTGGGGGTCAATGAAGCTTGTGGGAACAT	634

Db	129	ACTTTTGTCTCTCCTCCTGAGGTGTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAATAT	188
QY	635	TCGTGTGATCGTGGCAATAGCCAAAGAAATCTGCACCTACCCCATGTACTTTTCAT	694
Db	189	CTTAGTGAATGTGGCAATAGCCAAAGAAATCTGCATCTACCCCATGTACTTTTCAT	248
QY	695	CTGTAGCCTGGCTGTGGCCGATATGCTGTGAGCGTTTCCAAAGGCTCAGAGACCATCGT	754
Db	249	CTGCAGCTTGGCTGTGGCTGATATGCTGTGAGCGTTTCAATGGATCAGAAACCAATAT	308
QY	755	CATCACCTTGTGAACAGTACGGATACGGACCGCAGAGTTTTCACGGTGAATATTGATAA	814
Db	309	CATCACCTTATTAACAGTACAGATACGGATGCACAGAGTTTTCACAGTGAATATTGATAA	368
QY	815	TGTCATTGACTCGGTGATCTGTAGCTCCTTGTGCTGCCTCGATTTGAGCCCTGCTCTCAAT	874
Db	369	TGTCATTGACTCGGTGATCTGTAGCTCCTTGTGCTGCATTCATTTGAGCCCTGCTCTCAAT	428
QY	875	TGCAGTGGACAGTACTTTTACTTATCTTTTATGCCCTCCAGTACCATTAACATCATGACGT	934
Db	429	TGCAGTGGACAGTACTTTTACTTATCTTTCTATGCTCTCCAGTACCATTAACATCATGACGT	488
QY	935	GAGCGGGTTGGGATCATCATCAGTTGCTGTGGCGGCTTGCACGGTGTACAGGCACTTT	994
Db	489	TAAGCGGGTTGGGATCATCATTAAGTTGTATCTGGGCAGCTTGCACGGTTTCAGGCACTTT	548
QY	995	GTTTCATCATTTACTCGGACAGTACTGCTGCTCATCTGCTCCCTCATCACCATGTTCTTCA	1054
Db	549	GTTTCATCATTTACTCAGATAGTAGTCTGCTCATCATCTGCTCCCTCATCACCATGTTCTTCA	608
QY	1055	CATGCTGGCCCTCATGGCTTCTCTCTACCTGCACATGTTCCCTCATGGCCAGACTGCACAT	1114
Db	609	CATGCTGGCTCTCATGGCTTCTCTCTATGTCACATGTTCTGATGGCCAGGCTTCACAT	668
QY	1115	CAAGAGATTCGCCGTCTCTCCCGGCAACCGCACCATTCGCCCAAGGGGCCAACATGAAGGG	1174
Db	669	TAAGAGGATTCGCTCTCTCCCGGCACTGCTGCCATTCGCCCAAGGTGCCAATATGAAGGG	728
QY	1175	TGCCATTACCTTGACCATACACTCATTTGGGGTCTTCGCTGCTGCTGGGCTCCATTTCTCT	1234
Db	729	AGCGATTACCTTGACCATACCTCATTTGGGGTCTTCGCTGCTGCTGGGCTCCATTTCTCT	788
QY	1235	CCACTTGTATTTCTACATCTCTTGTCCCGCAAGTCCATCTGCTGCTGCTCATGCTCA	1294
Db	789	CCACTTGTATTTCTACATCTCTTGTCCCGCAAGTCCATCTGCTGCTGCTCATGCTCA	848
QY	1295	CTTTAACTTGTACCTCATTTCTGATCATGCTGTAACCTCCATFCATCGACCCCTCTCATTTATGC	1354
Db	849	CTTTAACTTGTATCTCATACTCATGATCATGTAATCAATCATCGATCCCTCTGATTTATGC	908
QY	1355	ACTCCGGAGCCAAAGAGTGGAGAAACCTTCAAGAGATCATCTGTTGCTATCCTCTGGG	1414
Db	909	ACTCCGGAGTCAAGAACTGAGGAAACCTTCAAGAGAGATCATCTGTTGCTATCCTCTGGG	968
QY	1415	TGGCCTTGTGACTTGTCTAGCAGATA	1441
Db	969	AGGCCTTGTGACTTGTCTAGCAGATA	995
RESULT 13			
AAAX75829			
ID	AAAX75829 standard; DNA; 996 BP.		
XX	AAAX75829;		
XX	22-JAN-2001 (first entry)		
XX	DNA encoding a human melanocortin-4 receptor polypeptide.		
DE	Human; melanocortin-1 receptor; melanocortin-2 receptor; 16q24.3;		
KW	18p11.2; melanocortin-3 receptor; 20q13.2; melanocortin-4 receptor;		
KW	18q21.3; melanocortin; ds.		



```
PR 26-FEB-1999; 9905-0121852.
PR 12-MAR-1999; 9905-0123944.
PR 12-MAR-1999; 9905-0123945.
PR 12-MAR-1999; 9905-0123946.
PR 12-MAR-1999; 9905-0123948.
PR 12-MAR-1999; 9905-0123949.
PR 12-MAR-1999; 9905-0123951.
PR 28-MAY-1999; 9905-0136436.
PR 28-MAY-1999; 9905-0136437.
PR 28-MAY-1999; 9905-0136439.
PR 28-MAY-1999; 9905-0137127.
PR 28-MAY-1999; 9905-0137131.
PR 28-MAY-1999; 9905-0137567.
PR 30-JUN-1999; 9905-0141448.
PR 27-AUG-1999; 9905-0151114.
PR 03-SEP-1999; 9905-0152524.
PR 29-SEP-1999; 9905-0156633.
PR 29-SEP-1999; 9905-0156655.
PR 29-SEP-1999; 9905-0156634.
XX
PA (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI: 2000-317986/27.
XX P-PSDB; AAB02845.
XX
XX Non-endogenous, human G protein-coupled receptors for screening
XX receptor, inverse or partial agonists useful as therapeutic agents -
XX Example 1; Page 132-133; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably
XX human G protein coupled receptors (GPCR), for which the endogenous
XX ligand is unknown (orphan GPCR receptors). More specifically the present
XX invention relates to non-endogenous, constitutively activated versions
XX of a human GPCR. These non-endogenous human GPCRs can be useful for
XX the direct identification of candidate compounds as receptors agonists,
XX inverse agonists or partial agonists for use as pharmaceutical agents.
XX AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
XX the exemplification of the present invention.
XX
XX Sequence 999 BP; 229 A; 243 C; 214 G; 313 T; 0 other;
XX
XX Query Match 41.2%; Score 817.2; DB 21; Length 999;
XX Best Local Similarity 89.1%; Pred. No. 1.1e-183;
XX Matches 882; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 455 CACCCCTTCACGACGGGAATCACACTTCTCTCCACTTCTGGAAACCGCAGCACCTACGGACA 514
Db 9 CTCACCCACCGTGGGATGCACACTTCTCTGACCTCTGGAACCGCAGCTACAGACT 68
QY 515 GCACGGCAACGCCACTGACTCCCTTGGCAAGGCTACCCCGAGGGGGATGCTACGACA 574
Db 69 GCACGAATGCTGAGTGCTCTGGAAAGGCTACTCTGATGGAGGGTGTACGACGA 128
QY 575 ACTCTTCGCTCCCCGGAGGTTCGTGACTCTGGGGGTCAATAAGCTTCTGGAGAACAT 634
Db 129 ACTTTTGTCTCTCGTAGGTGTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAAAT 188
QY 635 TCTGGTGATCGTGGCAATAGCCAAAGAAATCTGCACCTACCCCATGACTTTTTCAT 694
Db 189 CTTAGTGATTGTGGCAATAGCCAAAGAAATCTGCATTCACCCATGACTTTTTCAT 248
QY 695 CTGTAGCCCTGGCTGTGGCCGATATGCTGTGAGCGTTTCCACGGGTACAGACCATCGT 754
Db 249 CTGACGCTTGGCTGTGGCTGTATGCTGTGAGCGTTTCAATGATGACAGAACATTAT 308
QY 755 CATCACCCCTGTTGAACAGTACCGGATACGGACGCGGAGAGTTTACGGTGAATATTGATAA 814
Db 309 CATCACCCCTATTAAACAGTACAGATACGGATGCACAGAGTTTCACAGTGAATATTGATAA 368
XX
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QY 815 TGTCAATGACTCGGTGATGCTGTAGCTCCTTGTCTGCTCGCTCGATTGTCAGCTGCTCTCAAT 874
Db 369 TGTCAATGACTCGGTGATGCTGTAGCTCCTTGTCTGCTCGCTCGATTGTCAGCTGCTCTCAAT 428
QY 875 TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGTT 934
Db 429 TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCTCCAGTACCATAACATCATGACGTT 488
QY 935 GAGGCGGGTGGGATCATCATGATGCTATCTGGGGGCTTGCACCGGTGTCAGGCACTTT 994
Db 489 TAGCGGGTGGGATCAGCATAGTTGTATCTGGGGAGCTTGCACCGTTTCAGGCACTTT 548
QY 995 GTTCATCATTTACTCGGACAGTACTGCTGTCACTCATCTGCCTCATCACCATGTTCTTCAC 1054
Db 549 GTTCATCATTTACTCAGATAGTAGTCTGTCTCATCATCTGCCCTCATCAOCCATGTTCTTCAC 608
QY 1055 CATGCTGGCCCTCATGCGCTTCTCTCTACGTCACATGTTCTCTCATGCGGACAGTGCACAT 1114
Db 609 CATGCTGGCTCTCATGGCTTCTCTCTATGTCCACATGTTCTCTCATGCGGACAGTGCACAT 668
QY 1115 CAAGAGAATCGCGCTCCTCCGGGCACCGCACCATCCGCCAAGGGGCCCAACATGAAGG 1174
Db 669 TAGAGGATGCTGCTCCTCCCGGCACTGTGCGCATCCCGCAGGTGCCAATATGAAGG 728
QY 1175 TGCCATTACTTTGACCATACTCATTTGGGGTCTTCTGCTGCTGCTGGGCTTCCATTTCTCT 1234
Db 729 AGCGATTACTTTGACCATCTCATTTGGCGCTTTTGTGCTGCTGGGCCCCCATTTCTCT 788
QY 1235 CCACCTTGATTTCTACATCTCTTGTCCCGAGAAATCCATPACTGTGTGTGCTTCTCATGTCTCA 1294
Db 789 CCACCTTAATATTCTACATCTCTTGTCTCAGAATCCATATTGTGTGTGCTTCTCATGTCTCA 848
QY 1295 CTTTAACCTGTACCTCATCTCATGTAACCTCATCATCGACCCCTCATTTTATGC 1354
Db 849 CTTTAACCTGTATCTCATPACTCATCATGTATTAATCAATCATCGATCTCTCATTTATGC 908
QY 1355 ACTCGGGAGCCAGAGCTGAGGAAACCTTCAAAGAGATCATCTGTGTATCTCTCTGGG 1414
Db 909 ACTCGGGAGCTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTGTATCTCTCTGGG 968
QY 1415 TGGCCTTTGTGACTTGTCTAGCAGATACATA 1444
Db 969 AGGCGCTTTGTGACTTGTCTAGCAGATATTA 998
XX
RESULT 15
AAD25897 standard; cDNA; 999 BP.
XX
AC AAD25897;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human melanocortin 4-receptor (MC4R) cDNA.
XX
XX Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
KW MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
KW ASO; gene therapy; anorectic; chromosome 18q22; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace (307, G)
FT /*tag= a
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace (527, T)
FT /*tag= b
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace (594, T)
FT /*tag= c
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace (606, A)
FT /*tag= d
```



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FT      replace (751, C)
FT      /*tag= e
XX      /standard_name= "Single nucleotide polymorphism"
PN      WO200179222-A2.
XX      25-OCT-2001.
XX      12-APR-2001; 2001WO-US11943.
XX      12-APR-2000; 2000US-196677P.
XX      (GENA-) GENAISSANCE PHARM INC.
XX      Bentivegna SC, Choi JV, Kazemi A, Lee HH, Nandabalan K, Parks KE;
PI      Sausker EA;
XX      WPI; 2002-082744/11.
DR      P-PSDB; AAE15746.
XX      Novel polymorphic variants of melanocortin 4-receptor gene useful in
PT      studying expression and function of the protein, useful for screening
PT      candidate drugs to treat diseases related to the protein activity e.g.
PT      obesity
XX      Claim 24; Fig 2; 53pp; English.
XX      The invention relates to single nucleotide polymorphisms (SNP) in human
CC      melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful
CC      for improving the efficiency and reliability of several steps in the
CC      discovery and development of drugs for treating diseases associated
CC      with MC4R activity, e.g. obesity. MC4R gene is useful in studying the
CC      expression and function of MC4R and in expressing MC4R protein for
CC      use in screening for candidate drugs to treat diseases related to
CC      MC4R activity and in studying the effect of the variation on the
CC      biological activity of MC4R as well as on the binding affinity of
CC      candidate drugs targeting MC4R for the treatment of obesity. MC4R
CC      antibody is useful in a variety of diagnostic and prognostic formats
CC      and in therapeutic methods. Allele-specific oligonucleotide (ASO) is
CC      useful as probes and primers, and for assaying a polymorphism in
CC      MC4R gene. MC4R DNA is used in gene therapy. The present sequence is
CC      human MC4R cDNA. MC4R gene is located on chromosome 18q22.
XX      Sequence 999 BP; 229 A; 243 C; 214 G; 313 T; 0 other;
XX      Query Match      41.2%; Score 817.2; DB 24; Length 999;
XX      Best Local Similarity 89.1%; Pred. No. 1.le-183;
XX      Matches 882; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
XX      455 CACGCTTCAGCAGCGAATGCACACTTCTCTCCACTTCTGGAAACCGCAGCACCTACGGACA 514
XX      9 CTCACCCACCGTGGGATGCACACTTCTCTGCACCTCTGGAAACCGCAGCTTACAGACT 68
XX      515 GCACGGCAACGCCACTAGTCCCTTGGCAAAAGGCTACCCGACGGGGGATGCTACGAGCA 574
XX      69 GCACAGCAATGCCAGTCCCTTGGAAAGGCTACTCTGATGGAGGGTCTACGAGCA 128
XX      575 ACTCTTGTCTCCCGGAGGTGTCGTGACTCTGGGGTCTAAGCTTGTGGAGACAT 634
XX      129 ACTTTTGTCTCTCTCTGAGGTGTTTGTGACTCTGGGTGTCATCAGCTTGTGGAGAAAT 188
XX      635 TCTGGTGTCTGTCATAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 694
XX      189 CTTAGTATGTTGGCAATAGCCAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 248
XX      695 CTGTAGCTGCTGTGGCCGATATGCTGGTGGAGGTTTCCAAACGGGTGACAGACCATCGT 754
XX      249 CTGCAGCTTGGCTGTGCTGATATGCTGGTGGAGGTTTCAATGGATCAGAAACCATAT 308
XX      755 CATCACCCCTGTTGAACAGTAGCGATACGGAGCCGACGAGTTTACGGTGAATATTGATAA 814
XX      309 CATCACCCCTATTAAACAGTAGAGATACGGATACGGATGACAGAGTTTACAGTGAATATTGATAA 368
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Qy      815 TGTCAATTCACATCGGTGATCTAGTCTCTTGTCTGGCCTCGATTTGACAGCCTGCTCTCAAT 874
Db      369 TGTCAATTCACATCGGTGATCTAGTCTCTTGTCTGGCCTCGATTTGACAGCCTGCTCTCAAT 428
Qy      875 TGCAGTGGACAGGTACTTTACTATCTTTTATGCCCCCTCCAGTACCACATACATGACGGT 934
Db      429 TGCAGTGGACAGGTACTTTACTATCTTCTATGCTCTCCAGTACCACATATATGACAGT 488
Qy      935 GAGCGGGTTGGGATCATCATCAGTTCATCTGGCGGCTTGCAGAGGTGTCAGGATCTT 994
Db      489 TAAGCGGGTTGGGATCAGCATAAAGTTGATCTGGGACGCTTGCAGGTTTTCAGGATTTT 548
Qy      995 GTTCATCATTTACTCGGACACACTGCTGTGTCATCATCTGCTCATCATCACCATTGTTTTCAC 1054
Db      549 GTTCATCATTTACTCAGATAGTAGTGTGTCATCATCTGCTCATCACCATTGTTTTCAC 608
Qy      1055 CATGCTGGCCCTCATGGCTTCTCTACGTCCACATGTTCTCATGCGCAGACATGACAT 1114
Db      609 CATGCTGGCTCTCATGGCTTCTCTATGTCACATGTTCTGATGGCCAGGCTTCACAT 668
Qy      1115 CAAGAGATCGCCCTCTCCCGGCGCACCATCCGCCAAGGGGCAACATCAAGGG 1174
Db      669 TAAGAGGATGCTGTCTCTCCCGGCACTGGTGCCCATCCGCAAGTGCCCAATATGAAGGG 728
Qy      1175 TGCCATTACCTTGACCATACTATTGGGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1234
Db      729 AGCATTTACCTTGACCATCTGATTTGGGCTCTTGTGTCGTCGTCGTCGTCGTCGTCGTCGTC 788
Qy      1235 CCACCTTGATATTTACATCTCTTGTGCCAGAAATCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 1294
Db      789 CCACCTTAATATTTACATCTCTTGTGCCAGAAATCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 848
Qy      1295 CTTTAACTTGTACCTCATCTGATCATCTGTAACCTTCACTCCATCATCGACCTCTCATTTATGC 1354
Db      849 CTTTAACTTGTATCTCATACTGATCATGTGTAATTCATCATCGATCTCTGATTTATGC 908
Qy      1355 ACTCCGGAGCCAAGAGCTGAGGAAACCTTCAAAGAGATCATCTGTTGCTATCTCTCTGGG 1414
Db      909 ACTCCGGAGTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTTGCTATCCCTGGG 968
Qy      1415 TGGCCTTGTGACTTGTCTAGCAGATATA 1444
Db      969 AGGCTTTGTGACTTGTCTAGCAGATATA 998
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Search completed: June 14, 2003, 11:52:41

Job time : 335 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 18:03:31 ; Search time 51 seconds  
(without alignments)  
867.435 Million cell updates/sec

Title: US-09-884-211a-4

Perfect score: 1726

Sequence: 1 MNSTLQHGHTSLHFWNRST.....FKETICCYPLGLCLLSRY 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1726	100.0	332	AAU76428	Canine melanocortin
2	1685	97.6	332	AAU76427	Feline melanocortin
3	1638.5	94.9	332	AAW19704	Melanocortin-4 rec
4	1638.5	94.9	332	AAW79687	Melanocortin-4 rec
5	1638.5	94.9	332	AAW33724	Human melanocortin
6	1638.5	94.9	332	AAW92442	Human MC4 protein.
7	1638.5	94.9	332	AAW18769	A human melanocortin
8	1638.5	94.9	332	AAW83185	Synthetic labeled
9	1638.5	94.9	332	AAW68490	Amino acid sequenc
10	1632.5	94.6	332	AAW02845	Human G protein co

11	1632.5	94.6	332	AAE15746	Human melanocortin
12	1627.5	94.3	332	AAW02857	Human G protein co
13	1624.5	94.1	332	AAV94301	Rhesus monkey mela
14	1615.5	93.6	332	AAW83182	Melanocortin recep
15	1596.5	92.5	332	AAW87415	Melanocortin-4 rec
16	1592.5	92.3	332	AAW37831	Human melanocortin
17	1592.5	92.3	332	AAW42377	Homo sapiens mutan
18	1592.5	92.3	332	AAW87869	Human melanocortin
19	1590.5	92.1	332	AAW42378	Homo sapiens mutan
20	1583.5	91.7	332	AAW42379	Homo sapiens mutan
21	1463	84.8	311	AAU08750	Human melanocortin
22	1405	81.4	293	AAW83184	Melanocortin recep
23	1262	73.1	248	AAW78931	Porcine melanocort
24	1257	72.8	248	AAU08751	Porcine melanocort
25	1246	72.2	248	AAW78932	Porcine melanocort
26	1041	60.3	325	AAW79501	Rat melanocortin r
27	1026.5	59.5	325	AAW37833	Mouse melanocortin
28	1026.5	59.5	325	AAW87870	Mouse melanocortin
29	1025.5	59.4	325	AAW94266	Rhesus monkey mela
30	1023.5	59.3	325	AAW19705	Melanocortin-5 rec
31	1023.5	59.3	325	AAW79688	Melanocortin-5 rec
32	1023.5	59.3	325	AAW41067	Mouse melanocortin
33	1023.5	59.3	325	AAW33725	Mouse melanocortin
34	1023.5	59.3	325	AAW92443	Mouse MC5 protein.
35	1023.5	59.3	325	AAW18770	A human melanocort
36	1022.5	59.2	325	AAW79502	Human melanocortin
37	996.5	57.7	325	AAW49726	Sequence of a poly
38	994	57.6	323	AAW94427	Rhesus monkey mela
39	994	57.6	323	AAW60968	Murine melanocorti
40	994	57.6	323	AAE20595	Mus musculus melan
41	982.5	56.9	360	AAU95520	Human olfactory an
42	981.5	56.9	360	AAW19703	Melanocortin-3 rec
43	981.5	56.9	360	AAW79686	Melanocortin-3 rec
44	981.5	56.9	360	AAW33723	Human melanocortin
45	981.5	56.9	360	AAW92441	Human MC3 protein.

#### ALIGNMENTS

RESULT 1

AAU76428

ID AAU76428 standard; Protein; 332 AA.

XX AC AAU76428;

XX DT 08-MAY-2002 (first entry)

XX DE Canine melanocortin 4 receptor (MC4R).

XX KW Melanocortin 4 receptor; MC4R; G-protein coupled receptor; dog;

XX KW appetite; metabolic disorder; cachexia; anorexia;

XX KW weaning-induced inappetence; growth; diabetes; cancer; renal failure;

XX KW cardiac disease; endotoxaemia; fever; hepatic lipidosis; infection;

XX KW inflammation; post partum sow; dairy cow; livestock; poultry;

XX KW shipping stress; crowding stress; obesity; vaccine.

XX OS Canidae.

XX EPI167386-A1.

PN PN 02-JAN-2002.

PD PD 26-JUN-2001; 2001EP-0305509.

XX PF 26-JUN-2000; 2000US-213909P.

XX PR (PFIZ ) PFIZER PROD INC.

PA Hickman MA, Houseknecht KL, Robertson AS;

XX PI WPI; 2002-156598/21.

DR N-PSDB; ABK15578.

XX Novel canine or feline melanocortin 4 receptor polypeptide for  
PT screening modulator compounds useful for treating cachexia, anorexia,  
PT diabetes and cancer  
XX  
PT  
XX  
PS Claim 22; Fig 4; 73pp; English.  
XX  
XX The invention describes a substantially pure canine or feline  
CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be  
CC used in the treatment of appetite-related or metabolic disorders  
CC including cachexia, anorexia or weaning-induced inappetence and growth  
CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,  
CC fever, hepatic lipodosis, infection or inflammation, in a post partum  
CC sow, dairy cow, companion animal, livestock animal, poultry animal,  
CC animal suffering from shipping or crowding stress, lactating animal,  
CC obese animal or a gravid animal. (I) is useful in the generation of  
CC antibodies, as reagents in diagnostic assays, identification of other  
CC cellular gene products involved in the regulation of appetite in animals,  
CC as reagents in assays for screening for compounds that can be used in the  
CC treatment of appetite disorders in animals. A ligand of MC4R is useful  
CC for elaborating the biological function of MC4R gene product and for  
CC ameliorating appetite disorders and metabolic disorders, in animals. This  
CC is the amino acid sequence of the canine melanocortin 4 receptor (MC4R).  
CC a G-protein coupled receptor described in the method of the invention.  
XX  
XX Sequence 332 AA:  
XX  
XX Query Match 100.0%; Score 1726; DB 23; Length 332;  
XX Best Local Similarity 100.0%; Pred. No. 7.2e-180;  
XX Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYEQLFVSPVFTLVGISLL 60  
Db 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYEQLFVSPVFTLVGISLL 60  
QY 61 ENILVIVATAKNNLHSPMYFFTCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120  
Db 61 ENILVIVATAKNNLHSPMYFFTCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120  
QY 121 IDNVDSVICSLLASICSLLSTAVDRYFTIFVALQYHNMVRRVGGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASICSLLSTAVDRYFTIFVALQYHNMVRRVGGIIISCIWAACVTS 180  
QY 181 GILFIYSDSTAVIICLTMTFTMLMALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GILFIYSDSTAVIICLTMTFTMLMALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
QY 241 MKGATLTLLIGVVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
Db 241 MKGATLTLLIGVVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
QY 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332  
Db 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332  
RESULT 2  
AAU76427  
ID AAU76427 standard; Protein; 332 AA.  
XX  
AC AAU76427;  
XX  
XX  
DT 08-MAY-2002 (first entry)  
DE Feline melanocortin 4 receptor (MC4R).  
XX  
XX Melanocortin 4 receptor; MC4R; G-protein coupled; receptor; cat;  
KW appetite; metabolic disorder; cachexia; anorexia;  
KW weaning-induced inappetence; growth; diabetes; cancer; renal failure;  
KW cardiac disease; endotoxaemia; fever; hepatic lipodosis; infection;  
KW inflammation; post partum sow; dairy cow; livestock; poultry;  
KW shipping stress; crowding stress; obesity; vaccine.  
XX

OS Felidae.  
XX  
PN EP1167386-A1.  
XX  
PD 02-JAN-2002.  
XX  
XX 26-JUN-2001; 2001EP-0305509.  
XX  
PF 26-JUN-2000; 2000US-213909P.  
PR  
XX (PFIZ ) PFIZER PROD INC.  
PA  
XX Hickman MA, Houseknecht KL, Robertson AS;  
PI WPI: 2002-156598/21.  
XX N-PSDB; ABK15577.  
DR  
DR Novel canine or feline melanocortin 4 receptor polypeptide for  
PT screening modulator compounds useful for treating cachexia, anorexia,  
PT diabetes and cancer  
XX  
XX Claim 3; Fig 3; 73pp; English.  
XX  
XX The invention describes a substantially pure canine or feline  
CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be  
CC used in the treatment of appetite-related or metabolic disorders  
CC including cachexia, anorexia or weaning-induced inappetence and growth  
CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,  
CC fever, hepatic lipodosis, infection or inflammation, in a post partum  
CC sow, dairy cow, companion animal, livestock animal, poultry animal,  
CC animal suffering from shipping or crowding stress, lactating animal,  
CC obese animal or a gravid animal. (I) is useful in the generation of  
CC antibodies, as reagents in diagnostic assays, identification of other  
CC cellular gene products involved in the regulation of appetite in animals,  
CC as reagents in assays for screening for compounds that can be used in the  
CC treatment of appetite disorders in animals. A ligand of MC4R is useful  
CC for elaborating the biological function of MC4R gene product and for  
CC ameliorating appetite disorders and metabolic disorders, in animals. This  
CC is the amino acid sequence of the feline melanocortin 4 receptor (MC4R).  
CC a G-protein coupled receptor described in the method of the invention.  
XX  
XX Sequence 332 AA:  
XX  
XX Query Match 97.6%; Score 1685; DB 23; Length 332;  
XX Best Local Similarity 97.6%; Pred. No. 2.2e-175;  
XX Matches 324; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYEQLFVSPVFTLVGISLL 60  
Db 1 MNSTLQHGHTSLHFWNRSTYQHGHNATESLGKGYDPGCGYEQLFVSPVFTLVGISLL 60  
QY 61 ENILVIVATAKNNLHSPMYFFTCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120  
Db 61 ENILVIVATAKNNLHSPMYFFTCISLAVADMVLSVNSGSETIVITLLNSTDDAQSFYN 120  
QY 121 IDNVDSVICSLLASICSLLSTAVDRYFTIFVALQYHNMVRRVGGIIISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASICSLLSTAVDRYFTIFVALQYHNMVRRVGGIIISCIWAACVTS 180  
QY 181 GILFIYSDSTAVIICLTMTFTMLMALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
Db 181 GILFIYSDSTAVIICLTMTFTMLMALMASLVVHMFMLARLHKRIAVLPGTGTIRQGAN 240  
QY 241 MKGATLTLLIGVVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
Db 241 MKGATLTLLIGVVFVVCWAPFLLHLIFYISCPQNPYCVCFMSHFNLYLLIMCNSIIDPL 300  
QY 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332  
Db 301 IYALRSQELRKTFFKEIICCYPLGGLCDLSSRY 332  
RESULT 3

AAW19704  
ID AAW19704 standard; Protein; 332 AA.

XX AC AAW19704;

XX DT 19-AUG-1997 (first entry)

XX DE Melanocortin-4 receptor.

XX KW Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;  
KW pro-opiomelanocortin; adrenal cortical function; behaviour; learning;  
KW memory; cardiovascular system; analgesia; thermoregulation; prolactin;  
KW neurohumoral agent; biogenic amine.

XX OS Homo sapiens.

XX PN US5622860-A.

XX PD 22-APR-1997.

XX PF 17-FEB-1994; 94US-0200711.

XX PR 17-FEB-1994; 94US-0200711.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Gantz I, Yamada T;

XX DR WPI; 1997-244394/22.

XX DR N-PSDB; AAT68790.

XX PT Nucleic acid molecules encoding melanocortin receptors - useful to  
PT transfect mammalian cells lacking endogenous receptors to induce  
PT their expression

XX PS Claim 4; Column 43-46; 58pp; English.

XX AA W19703-W19707 represent the human and mouse melanocortin (MC)  
CC receptors. This sequence represents the MC4R, expressed primarily in  
CC brain, but absent in the adrenal cortex, melanocytes and placenta. The  
CC gene encoding this sequence is located at chromosome locus 18q21.3. MCs  
CC are products of pro-opiomelanocortin post-translational processing, and  
CC are known to have a broad array of physiological actions. MCs are known  
CC to have effects on adrenal cortical functions and on melanocytes, as well  
CC as affecting behaviour, learning, memory, control of the cardiovascular  
CC system, analgesia, thermoregulation and the release of other neurohumoral  
CC agents (such as prolactin and biogenic amines). The nucleic acids can be  
CC used to transfect mammalian cells lacking endogenous MC receptors to  
CC induce their expression. These sequences can also be used to screen and  
CC identify drugs which specifically react with MC4Rs on the surface of a  
CC cell. The drugs can then be used for treating diseases which have MC4Rs  
CC implicated as one of their causes. Vectors containing these sequences can  
CC also be used to treat the diseases.

XX SQ Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 18; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;

Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATSLGKGYPDGCGYEQLFVSPVFTLGVISLL 60

DB 2 VNST-HRCGMHTSLHFWNRSSYRLHNSASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60

QY 61 ENILVIVAIAKNKNLHSPWFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

DB 61 ENILVIVAIAKNKNLHSPWFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

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DB 121 IDNVDSVICSLLASCSLLSIAVDYFTTFYALQYHNIMTVRVGIIISCIWAACVTS 180

QY 181 GILFIYSDSTAIIICLTMTFTMLMASLYVHMFMLARLHKRIAVLPCTGTGAIROGAN 240

DB 181 GILFIYSDSTAIIICLTMTFTMLMASLYVHMFMLARLHKRIAVLPCTGTGAIROGAN 240

QY 241 MKGATLTILIGVFWVCHAPFLHLIFVYISCPQNYCYCFKSHFNLYLILIMCNSTIDPL 300

DB 241 MKGATLTILIGVFWVCHAPFLHLIFVYISCPQNYCYCFKSHFNLYLILIMCNSTIDPL 300

QY 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

DB 301 IYALRSQELRKTFKEIICCYPLGGLCDLSSRY 332

RESULT 4

AAW79687

ID AAW79687 standard; Protein; 332 AA.

XX AC AAW79687;

XX DT 17-DEC-1998 (first entry)

XX DE Melanocortin-4 receptor.

XX KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain;  
KW adrenal cortex; melanocyte; placenta.

XX OS Homo sapiens.

XX PN US5817787-A.

XX PD 06-OCT-1998.

XX PF 23-APR-1997; 97US-0842045.

XX PR 17-FEB-1994; 94US-0200711.

XX PR 27-JUN-1996; 96US-0672109.

XX PR 23-APR-1997; 97US-0842045.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Gantz I, Yamada T;

XX DR WPI; 1998-556471/47.

XX DR N-PSDB; AAW62352.

XX PT DNA encoding melanocortin-5 receptor - useful in hybridisation  
XX assays for melanocortin-5 receptor nucleic acids

XX PS Disclosure; Column 43-46; 58pp; English.

XX CC The present sequence represents the human melanocortin-4 (MC4) receptor,  
CC the gene of which has been localised to chromosome 18q21.3. This  
CC receptor is activated by both the amino and carboxyl terminal end amino  
CC acids of melanocortins and has been found to be expressed primarily in  
CC the brain and is absent from the adrenal cortex, melanocytes and  
CC placenta. The DNA sequence that produces this polypeptide was identified  
CC by using oligonucleotides constructed from previously identified  
CC receptors MC1 and MC3, this was performed by using these oligonucleotides  
CC to search genomic DNA for other members of the receptor family. These  
CC genes and their products may be used to provide therapeutic vehicles for  
CC the treatment of processes involving the function of melanocortin  
CC receptors.

XX SQ Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 19; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;

Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSLHFWNRSTYQHGHNATSLGKGYPDGCGYEQLFVSPVFTLGVISLL 60

DB 2 VNST-HRCGMHTSLHFWNRSSYRLHNSASESLGKGYSDGCGYEQLFVSPVFTLGVISLL 60

QY 61 ENILVIVAIAKNKNLHSPWFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAQSFTVN 120

|||||  
Db 61 ENILVIVAIKAKNKLHSPMYFFICSLAVADMLVSVNGSETIITLLNSTDTAQSTVN 120  
|||||  
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|||||  
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIIISCIIWAACVS 180  
|||||  
Qy 181 GILFIYSDSTAVIICLTMTFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGAIROGAN 240  
|||||  
Db 181 GILFIYSDSSAVIICLTMTFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGAIROGAN 240  
|||||  
Qy 241 MKGAITLTILIGVVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
|||||  
Db 241 MKGAITLTILIGVVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
|||||  
Qy 301 IYALRSOELRKTEKEIICCPYLGGLCDLSRY 332  
|||||  
Db 301 IYALRSOELRKTEKEIICCPYLGGLCDLSRY 332

## RESULT 5

AAW33724  
ID AAW33724 standard; Protein; 332 AA.

AC AAW33724;

XX 30-APR-1998 (first entry)

DT Human melanocortin-4 (MC4) receptor.

DE Human melanocortin receptor; ligand; MC4; human.

XX Homo sapiens.

OS US5703220-A.

PN 30-DEC-1997.

PD 27-JUN-1996; 96US-0671525.

PF 17-FEB-1994; 94US-0200711.

PR 27-JUN-1996; 96US-0671525.

XX (UNMI ) UNIV MICHIGAN.

XX Gantz I, Yamada T;

XX WPI; 1998-076484/07.

XX N-PSDB; AAV06400.

XX DNA encoding human melanocortin-4 receptor - and cells useful in

PT assay for MC4 receptor ligands

XX Claim 1; Columns 43-46; 59pp; English.

XX This is a human melanocortin receptor-4 (MC4). The MC4 receptor of this  
XX invention is activated by amino acids in the carboxyl and amino terminal  
XX portions of the heptapeptide sequence shared by all the melanocortin  
XX peptides. MC4 is expressed primarily in brain and is notably absent in  
XX the adrenal cortex, melanocytes and placenta. The MC4 receptor gene was  
XX localised to chromosome loci 18q21.3. The invention provides methods to  
XX identify ligands that bind to MC4 receptor.

XX Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 19; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;

Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MNSTLQHGMMHTSLHFWNRSTYGOHGNATESLGKYPDGGCYEQLFVSPFVTLGVISLL 60

Db 2 VNST-HRGMMHTSLHFWNRSTYGOHGNATESLGKYPDGGCYEQLFVSPFVTLGVISLL 60

Qy 61 ENILVIVAIKAKNKLHSPMYFFICSLAVADMLVSVNGSETIITLLNSTDTAQSTVN 120  
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Db 61 ENILVIVAIKAKNKLHSPMYFFICSLAVADMLVSVNGSETIITLLNSTDTAQSTVN 120  
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|||||  
Db 121 IDNVDSVICSSLLASICSLLSTAVDRYFTIFVALQYHNIMTVRRVGIIISCIIWAACVS 180  
|||||  
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|||||  
Db 181 GILFIYSDSSAVIICLTMTFFTMLALMASLYVHMFMLARLHKRIKRIAVLPGTGAIROGAN 240  
|||||  
Qy 241 MKGAITLTILIGVVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
|||||  
Db 241 MKGAITLTILIGVVFVVCWAPFFLHLIFYISCPQNPYCVCFMSHFNLILIMCNSIIDPL 300  
|||||  
Qy 301 IYALRSOELRKTEKEIICCPYLGGLCDLSRY 332  
|||||  
Db 301 IYALRSOELRKTEKEIICCPYLGGLCDLSRY 332

## RESULT 6

AAW92442  
ID AAW92442 standard; Protein; 332 AA.

XX AAW92442;

DT 21-APR-1999 (first entry)

XX Human MC4 protein.

DE Melanocortin-4 receptor; MC1; MC2; MC3; MC4; MC5; detection; probe;  
XX receptor binding; secondary signalling; tissue distribution.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..332 /note= "No stop codon given"

XX US5869257-A.

XX 09-FEB-1999.

XX 23-APR-1997; 97US-0842238.

XX 17-FEB-1994; 94US-0200711.

XX 27-JUN-1996; 96US-0671525.

XX 23-APR-1997; 97US-0842238.

XX (UNMI ) UNIV MICHIGAN.

XX Gantz I, Yamada T;

XX WPI; 1999-152760/13.

XX N-PSDB; AAX01964.

XX Probe for detecting melanocortin-4 receptor genes - that

PT specifically hybridises to defined DNA sequence

XX Example 1; Column 45-46; 60pp; English.

XX This sequence represents the human melanocortin-4 receptor, MC4. This  
XX protein is used in a method in which a nucleic acid probe useful for  
XX specifically detecting melanocortin-4 receptor genes is described.

XX This probe is used to isolate genes encoding melanocortin receptors,  
XX to characterise melanocortin receptor binding and secondary signalling  
XX and to determine tissue distribution of the melanocortin receptors.

XX Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 20; Length 332;

Best Local Similarity 95.5%; Pred. No. 2.6e-170;



Example 11; Page 71; 120pp; English.

New methods are described by which membrane polypeptides can be labelled. The method comprises chemoselective chemical ligation of the membrane polypeptide which is incorporated in a lipid matrix, and a ligation label. Both contain an amino acid having an unprotected reactive group that together undergo chemoselective ligation to form a covalent bond. The method can be used to label folded polypeptides embedded in a lipid membrane, by treating the polypeptide with a reagent that cleaves specifically adjacent to an amino acid with an unprotected reactive group and then ligating the cleaved polypeptide with the ligation label. The ligation label can be a chromophore, thus ligand binding to membrane bound polypeptides can be detected by contacting a membrane bound polypeptide comprising a chromophore, with the ligand under investigation and screening for binding in an assay characterized by detecting fluorescence resonance energy transfer (FRET) between the chromophore and a second chromophore, the chromophores comprising a donor and acceptor pair of a resonance energy transfer system. The methods are used for lipid matrix-assisted chemical ligation and synthesis of membrane polypeptides. Labeled membrane polypeptides are used to detect ligand binding and the identification of receptor domains, e.g. for structure/activity studies. They can also be used in drug screening, selection or design, and for diagnosis. The methods are particularly used for fluorescent resonance energy transfer (FRET) analysis of previously inaccessible membrane polypeptides. The method allows site-specific incorporation of labels during polypeptide synthesis and analysis of previously inaccessible membrane proteins. A Melanocortin receptor MC4 which also comprises a Factor Xa cleavage site (AAV83182) can be cleaved with Factor Xa to give a C-terminal alpha-thioester modified MC4 receptor ligation label (AAV83183) and an MC4 receptor membrane polypeptide cleavage product (AAV83184). Chemical ligation of cleaved MC4 in alternative membrane patches or micelles to an MC4 ligation label produces this synthetic labeled MC4 product (AAV83185).

Sequence 332 AA;

Query Match 94.9%; Score 1638.5; DB 21; Length 332;  
Best Local Similarity 95.5%; Pred. No. 2.6e-170;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MNSTLQHGHTSIHFNRSTYQHGHNATESLKGYPDGGCYBQLFVSPFVTLGVISLL 60  
DB 2 VNST-HRGHTSLHLNRSYRLHNSASBSLKGYSDDGGCYBQLFVSPFVTLGVISLL 60  
QY 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
DB 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVTCSSLLASICSLLSIAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180  
DB 121 IDNVDSVTCSSLLASICSLLSIAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180  
QY 181 GILFIYSDSTAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240  
DB 181 GILFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240  
QY 241 MKGAILTLTILGVVVCWAPFHLFIYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300  
DB 241 MKGAILTLTILGVVVCWAPFHLFIYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300  
QY 301 IVALRSQELRKTKEIICCYPLGGLCDLSSRY 332  
DB 301 IVALRSQELRKTKEIICCYPLGGLCDLSSRY 332

RESULT 9

AAB68490  
ID AAB68490 standard; Protein; 332 AA.  
XX  
AC AAB68490;  
XX

23-JUL-2001 (first entry)  
Amino acid sequence of a human melanocortin-4 receptor (MC-R4).  
Human; melanocortin-4 receptor; MC-R4; transgenic animal; body weight;  
food intake; obesity; diabetes; anorexia; cachexia; cancer;  
sexual dysfunction; pain; impaired memory; neuronal regeneration;  
neuropathy; growth disorder; growth hormone;  
insulin-like growth factor-1.  
Homo sapiens.  
XX  
XX WO200133956-A1.  
XX 17-MAY-2001.  
XX 13-NOV-2000; 2000WO-US31061.  
XX 12-NOV-1999; 99US-0165074.  
XX (MERI ) MERCK & CO INC.  
XX Van Der Ploeg LHT, Chen AS, Chen HY, Forrest MJ, MacIntyre DE;  
XX Metzger JM, Palyha OC, Feighner SD, Hreniuk D;  
XX WPI; 2001-343541/36.  
XX N-PSDB; AAF85465.  
XX New transgenic animal with non-functional gene for melanocortin-4  
XX receptor, useful for identifying specific modulators, potentially used  
XX for treating obesity or diabetes -  
XX Disclosure; Fig 2; 58pp; English.  
XX The present sequence represents a human melanocortin-4 receptor (MC-R4).  
XX The specification describes transgenic non-human animals whose somatic  
XX and germ cells contain at least one non-functional gene for MC-4R  
XX protein. The transgenic animals, or cells derived from them, are used  
XX to screen for compounds that modulate MC-4R. These modulators are  
XX potentially useful for regulating body weight and food intake and  
XX treatment of associated diseases, obesity; diabetes; anorexia; cachexia;  
XX cancer; sexual dysfunction; pain; impaired memory or neuronal  
XX regeneration; neuropathy; growth disorders linked to growth hormone  
XX and insulin-like growth factor-1. They can also be used to study MC-4R  
XX expression and activity.  
SQ Sequence 332 AA;  
Query Match 94.9%; Score 1638.5; DB 22; Length 332;  
Best Local Similarity 95.5%; Pred. No. 2.6e-170;  
Matches 317; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
QY 1 MNSTLQHGHTSIHFNRSTYQHGHNATESLKGYPDGGCYBQLFVSPFVTLGVISLL 60  
DB 2 VNST-HRGHTSLHLNRSYRLHNSASBSLKGYSDDGGCYBQLFVSPFVTLGVISLL 60  
QY 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
DB 61 ENILVIVATAKNNKLNHSPMYFFICSLAVADMVLSVNSGSETIVITLLNSTDTDAQSFTVN 120  
QY 121 IDNVDSVTCSSLLASICSLLSIAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180  
DB 121 IDNVDSVTCSSLLASICSLLSIAVDRYFTIFVALQYHNIMTVRRVGGIIISCIWAACVTS 180  
QY 181 GILFIYSDSTAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240  
DB 181 GILFIYSDSSAVIICLTIMFTMLMASLVHMFMLARLHKRIAVLPGTGTROGAN 240  
QY 241 MKGAILTLTILGVVVCWAPFHLFIYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300  
DB 241 MKGAILTLTILGVVVCWAPFHLFIYISCPQNPVCVCFMSHFNLYLLIMCNSTIDPL 300  
QY 301 IVALRSQELRKTKEIICCYPLGGLCDLSSRY 332







Db 121 IDNVDSVICSLLASICSLSIAVDRTTFYALQYHNIMTVKRVGSGISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVIICLTMTFTMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
Db 181 GILFIYSDSTAVIICLTMTFTMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
Qy 241 MKGAITLILIGVFWVWAPFLLHIFYISCPQNPYCVCFMSHFNLXILILMCSIIDPL 300  
Db 241 MKGAITLILIGVFWVWAPFLLHIFYISCPQNPYCVCFMSHFNLXILILMCSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGLDLSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGLDLSRY 332

## RESULT 13

AA94301  
ID AA94301 standard; Protein; 332 AA.

XX AC AA94301;

DT 04-AUG-2000 (first entry)

XX Rhesus monkey melanocortin-4 receptor protein.

XX Rhesus monkey; rhodopsin; G-protein coupled receptor; anorectic;  
KW melanocyte stimulating hormone; melanocortin receptor; obesity.

XX Macaca mulatta.

XX WO200027863-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-US25767.

XX 09-NOV-1998; 98US-0107721.

XX (MERI ) MERCK & CO INC.

XX MacNeill DJ, Weinberg DH, Van Der Ploeg LHT;

XX WPI; 2000-376480/32.

DR N-ESDB; AAA26972.

XX Novel DNA encoding rhesus monkey melanocortin 4 receptor protein,  
PT recombinant vectors and host cells, useful in methods for identifying  
PT selective agonists and antagonists

XX Claim 27; Page 35; 53pp; English.

XX The present sequence is the rhesus monkey melanocortin-4  
CC receptor protein (MC-4R). Melanocortin receptors belong to the rhodopsin  
CC sub-family of G-protein coupled receptors. They bind and are  
CC activated by peptides such as alpha-, beta-, or gamma-melanocyte  
CC stimulating hormones derived from the pro-opiomelanocortin gene and they  
CC are believed to mediate a wide range of physiological functions.  
CC The rhesus MC-4R gene was isolated by PCR using a series of four  
CC oligonucleotides (AAA26973-A26976) based on the human MC-4R gene sequence  
CC and designed to incorporate a restriction enzyme site for cloning into  
CC the expression vector pCI-neo. The recombinant vector was transformed  
CC into DH5a cells in preparation for DNA sequencing. The MC-4R gene  
CC sequence (AAA26972) or a mutated form may be introduced into an  
CC expression vector for expression in host cells. The subcellular  
CC membrane fractions will comprise either wild-type or mutant forms of  
CC rhesus MC-4R at enhanced levels and can be used in assays to identify  
CC ligand binding, activators and modulators, agonists and antagonists of  
CC MC-4R. This will allow for selection of compounds that are active for  
CC the rhesus receptor in vitro and will allow the selection of novel  
CC drugs to treat obesity.

XX Sequence 332 AA;

50

Query Match 94.1%; Score 1624.5; DB 21; Length 332;  
Best Local Similarity 94.6%; Pred. No. 8.9e-169;  
Matches 314; Conservative 7; Mismatches 10; Indels 1; Gaps 1;  
Qy 1 MNSTLQOHMHTSLHFWNRSTYQGRGNATSESLGKYPDGGCYEQLFVSPVFTLVISLL 60  
Db 2 VNST-HRGMHASLHLWNRSSHLNASESLGKYGSDGCEYEQLFVSPVFTLVISLL 60  
Qy 61 ENILVIVAIANKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDAOSFTVN 120  
Db 61 ENILVIVAIANKNLHSPMYFFICSLAVADMLVSVNSGSETIVITLLNSTDTDTOSFTVN 120  
Qy 121 IDNVDSVICSLLASICSLSIAVDRTTFYALQYHNIMTVKRVGSGISCIWAACVTS 180  
Db 121 IDNVDSVICSLLASICSLSIAVDRTTFYALQYHNIMTVKRVGSGISCIWAACVTS 180  
Qy 181 GILFIYSDSTAVIICLTMTFTMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
Db 181 GILFIYSDSTAVIICLTMTFTMLALMASLYVHMFMLARLHKRIAVLPCTGTROGAN 240  
Qy 241 MKGAITLILIGVFWVWAPFLLHIFYISCPQNPYCVCFMSHFNLXILILMCSIIDPL 300  
Db 241 MKGAITLILIGVFWVWAPFLLHIFYISCPQNPYCVCFMSHFNLXILILMCSIIDPL 300  
Qy 301 IYALRSQELRKTKEIICCYPLGGLDLSRY 332  
Db 301 IYALRSQELRKTKEIICCYPLGGLDLSRY 332

## RESULT 14

AA93182  
ID AA93182 standard; protein; 332 AA.

XX AC AA93182;

DT 24-JUL-2000 (first entry)

XX Melanocortin receptor MC4 comprising Factor Xa cleavage site.

XX Membrane polypeptide; lipid matrix; synthesis; ligation;  
KW chemoselective ligation; fluorescence resonance energy transfer;  
KW FRET; chromophore; ligand; receptor domain; drug screening;  
KW diagnosis; ion channel; melanocortin receptor; MC4.

XX Synthetic.

XX Homo sapiens.

XX WO200012536-A2.

XX 09-MAR-2000.

XX 26-AUG-1999; 99WO-US19542.

XX 31-AUG-1998; 98US-0144964.

XX 05-MAR-1999; 99US-0263971.

XX (GRYP-) GRYPHON SCI.

XX Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;

XX WPI; 2000-270792/23.

XX Selectively labeled membrane peptides, useful e.g. for detecting ligand  
PT binding to receptors and in drug screening, are prepared, in lipid  
PT matrix, by reaction between amino acid residues

XX Example 11; Page 68-69; 120pp; English.

XX New methods are described by which membrane polypeptides can be  
CC labelled. The method comprises chemoselective chemical ligation of  
CC the membrane polypeptide which is incorporated in a lipid matrix,  
CC and a ligation label. Both contain an amino acid having an  
CC unprotected reactive group that together undergo chemoselective



Db 301 IYALRSQELRKTKEIICCYPLGGICDLSSRY 332

Search completed: June 4, 2003, 18:15:43  
Job time : 52 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:25:54 ; Search time 210 Seconds  
(without alignments)

13687.622 Million cell updates/sec

Title: US-09-884-211A-2

Perfect score: 1985

Sequence: 1 ctaagaccgtgggaggcag.....gaataaaaaaaaaa 1985

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 72403093 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published\_Applications\_NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1985	100.0	1785	9	US-09-884-211A-2
2	1166.6	58.8	1908	9	US-09-884-211A-1
3	968.6	48.8	1950	9	US-09-910-180-1
4	939	47.3	1671	9	US-10-288-160-15
5	426	21.5	978	9	US-10-288-160-17
6	424.8	21.4	1650	12	US-10-052-545-15
7	406.6	20.5	1675	10	US-09-903-395-1
8	387.4	19.5	1338	9	US-10-288-160-11
9	306.6	15.4	1270	12	US-10-052-545-1
10	303.4	15.3	1633	9	US-10-288-160-5
11	279	14.1	1260	9	US-10-288-160-3
12	279	14.1	1260	10	US-09-815-944-19
13	275.4	13.9	2012	9	US-10-151-431-3
14	273.8	13.8	2012	9	US-10-288-160-7
15	252.8	12.7	1100	12	US-10-015-948-1
16	246	12.4	1108	9	US-10-151-431-5
17	241.2	12.2	1108	9	US-10-288-160-9
18	138.8	7.0	306	12	US-10-052-545-7
19	124.4	6.3	312	12	US-10-052-545-9

20	116.6	5.9	372	12	US-10-052-545-11	Sequence 11, Appl
21	106.2	5.4	200	10	US-09-903-395-4	Sequence 4, Appl
22	97.6	4.9	200	12	US-10-015-948-4	Sequence 4, Appl
23	83.8	4.2	285	12	US-10-052-545-5	Sequence 5, Appl
24	71.6	3.6	1146	9	US-10-028-156-7	Sequence 7, Appl
25	71.6	3.6	1146	9	US-10-029-401-7	Sequence 7, Appl
26	71.6	3.6	1146	9	US-10-029-372-7	Sequence 7, Appl
27	70.2	3.5	1137	12	US-10-037-616-3	Sequence 3, Appl
28	64.2	3.2	1062	10	US-09-771-063-3	Sequence 3, Appl
29	62.6	3.2	1062	9	US-10-084-507B-19	Sequence 19, Appl
30	62.6	3.2	1062	10	US-09-771-063-1	Sequence 1, Appl
31	62.6	3.2	1062	12	US-10-037-616-5	Sequence 5, Appl
32	62.6	3.2	1170	9	US-10-084-507B-16	Sequence 16, Appl
33	62.2	3.1	1032	9	US-09-971-228-2	Sequence 2, Appl
34	62.2	3.1	1089	10	US-09-993-844-14	Sequence 14, Appl
35	62.2	3.1	1149	9	US-09-971-228-1	Sequence 1, Appl
36	62.2	3.1	1149	9	US-09-759-514-1	Sequence 1, Appl
37	62.2	3.1	1376	9	US-09-971-228-4	Sequence 4, Appl
38	62.2	3.1	2776	12	US-10-037-616-1	Sequence 1, Appl
39	62.2	3.1	4063	9	US-10-092-154-1091	Sequence 1091, Ap
40	62.2	3.1	4063	10	US-09-764-847-1091	Sequence 1091, Ap
41	61.8	3.1	200	12	US-10-015-948-3	Sequence 3, Appl
c 42	60	3.0	583	10	US-09-864-761-20772	Sequence 20772, A
c 43	60	3.0	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c 44	59.8	3.0	364	9	US-10-084-507B-14	Sequence 14, Appl
45	59.8	3.0	388	9	US-09-796-692-3532	Sequence 3532, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-884-211A-2

; Sequence 2, Application US/09884211A

; Publication No. US20030032791A1

; GENERAL INFORMATION:

; APPLICANT: Alan et. al.

; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL

; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE

; FILE REFERENCE: PC10743A

; CURRENT APPLICATION NUMBER: US/09/884.211A

; CURRENT FILING DATE: 2000-06-26

; PRIOR FILING DATE: 60/213,909

; PRIOR FILING DATE: 2000-06-26

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 2

; LENGTH: 1985

; TYPE: DNA

; ORGANISM: Canine MC4R Nucleotide Sequence

US-09-884-211A-2

Query Match 100.0%; Score 1985; DB 9; Length 1985;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAGACCGTGGGAGGAGCAGCTGATGCGACATGTGCACGAGATTTCAGCTCTCTGGTGGC 60

|||||

Db 1 CTAAGACCGTGGGAGGAGCAGCTGATGCGACATGTGCACGAGATTTCAGCTCTCTGGTGGC 60

|||||

Qy 61 TCGGCGCAACTCGGAGAATTACTTGCACAGACCTCAGTCAATGCGCTAGACTAAAGTTT 120

|||||

Db 61 TCGGCGCAACTCGGAGAATTACTTGCACAGACCTCAGTCAATGCGCTAGACTAAAGTTT 120

|||||

Qy 121 AAGTGGGAGTGGAGGACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 180

|||||

Db 121 AAGTGGGAGTGGAGGACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 180

|||||

Qy 181 AAAAAAGCAAGACAGACACTCTTTGAAGTAAAGATGAGCATTTTCAGAAATCGAAGATGTTA 240

|||||

Db 181 AAAAAAGCAAGACAGACACTCTTTGAAGTAAAGATGAGCATTTTCAGAAATCGAAGATGTTA 240

|||||

QY 241 CAGTGAAGGTGATCGGAGCTGTACCTGGGAAGACAGTAAGAGCTCCACTGCCAGCCCTTTG 300  
DB 241 CAGTGAAGGTGATCGGAGCTGTACCTGGGAAGACAGTAAGAGCTCCACTGCCAGCCCTTTG 300  
QY 301 GAGCAGGGACAGGTACTCAACACCTGGCAGGCCAGCTGGATCCTCAGAACCTTTGGGACG 360  
DB 301 GAGCAGGGACAGGTACTCAACACCTGGCAGGCCAGCTGGATCCTCAGAACCTTTGGGACG 360  
QY 361 CACGGAGAGGGGGAACATCATCCGGGGCTCCCTGGCTGGAGAGGGCCGAATCAGTCCCGA 420  
DB 361 CACGGAGAGGGGGAACATCATCCGGGGCTCCCTGGCTGGAGAGGGCCGAATCAGTCCCGA 420  
QY 421 GGGGCTGTCATACACTTTGTCAGATGAATCTCCACCCCTTCAGCAGCGAAATGCAACAT 480  
DB 421 GGGGCTGTCATACACTTTGTCAGATGAATCTCCACCCCTTCAGCAGCGAAATGCAACAT 480  
QY 481 CTCCTCACCTTCGGAACCGCAGCACCTACGGGACAGCAGCGCAACCGCACTGAGTCCCTTG 540  
DB 481 CTCCTCACCTTCGGAACCGCAGCACCTACGGGACAGCAGCGCAACCGCACTGAGTCCCTTG 540  
QY 541 GCAAAGGCTTACCCGACGGGGATGCTACGAGCAACTCTTCTGCTCCCGGAGGTGTTGG 600  
DB 541 GCAAAGGCTTACCCGACGGGGATGCTACGAGCAACTCTTCTGCTCCCGGAGGTGTTGG 600  
QY 601 TGACTCTGGGGTCAATAGCTTGCCTGGAGAACATCTCGTGATCGTGGCAATAGCCAAGA 660  
DB 601 TGACTCTGGGGTCAATAGCTTGCCTGGAGAACATCTCGTGATCGTGGCAATAGCCAAGA 660  
QY 661 ACAAGAATCTGCACATCACCATGTACTTTTTCATCTGTAGCCTGGCTGCGCGGATATGC 720  
DB 661 ACAAGAATCTGCACATCACCATGTACTTTTTCATCTGTAGCCTGGCTGCGCGGATATGC 720  
QY 721 TGGTGAGGCTTTCACACGGGTGAGAGACATCGTCACTCACCTGTTGAACAGTACGGATA 780  
DB 721 TGGTGAGGCTTTCACACGGGTGAGAGACATCGTCACTCACCTGTTGAACAGTACGGATA 780  
QY 781 CGGACGGCAGAGTTTACGGTGAATATGTAATGTCATTTGACCTCGGTGATCTAGCT 840  
DB 781 CGGACGGCAGAGTTTACGGTGAATATGTAATGTCATTTGACCTCGGTGATCTAGCT 840  
QY 841 CCTTCTGCGCTCGATTTGACGCTGCTCAATTTGACGAGTGGACAGGTACTTTACTATCT 900  
DB 841 CCTTCTGCGCTCGATTTGACGCTGCTCAATTTGACGAGTGGACAGGTACTTTACTATCT 900  
QY 901 TTTATGCGCTCCAGTACCATACATCATGACGGTGAGCGGTTGGGATCATCATCAGTT 960  
DB 901 TTTATGCGCTCCAGTACCATACATCATGACGGTGAGCGGTTGGGATCATCATCAGTT 960  
QY 961 GCATCTGGCGGCTTGCAGGCTGTCAGGATCTTGTTCATCATTTACTCGGACACTG 1020  
DB 961 GCATCTGGCGGCTTGCAGGCTGTCAGGATCTTGTTCATCATTTACTCGGACACTG 1020  
QY 1021 CTGTATCATCTGCTCATCATCATGTTCTTCCACCATGCTGGCCCTCATGGCTTCTCT 1080  
DB 1021 CTGTATCATCTGCTCATCATCATGTTCTTCCACCATGCTGGCCCTCATGGCTTCTCT 1080  
QY 1081 AGCTCCACATGTTCTTATGCGCAGACTGCATCAAGAGAAATCGCGTCTCCCGGCA 1140  
DB 1081 AGCTCCACATGTTCTTATGCGCAGACTGCATCAAGAGAAATCGCGTCTCCCGGCA 1140  
QY 1141 CCGGACCATTCGGCAAGGGCCCAACATGAAGGGTGCCATTTACCTTGACCATCATG 1200  
DB 1141 CCGGACCATTCGGCAAGGGCCCAACATGAAGGGTGCCATTTACCTTGACCATCATG 1200  
QY 1201 GGGTCTTCTGCTGCTGCGGCTCCATCTTCTCCCTCATTTTACATCTTCTCTCTGTC 1260  
DB 1201 GGGTCTTCTGCTGCTGCGGCTCCATCTTCTCCCTCATTTTACATCTTCTCTCTGTC 1260  
QY 1261 CCCAGAATCCACTGTTGCTGCTTCTCATGTTTAACTTGTACCTCATCTTGTATCA 1320  
DB 1261 CCCAGAATCCACTGTTGCTGCTTCTCATGTTTAACTTGTACCTCATCTTGTATCA 1320  
QY 1321 TGTGTAACCTCATCATCATGACCTCTCATTTATGCACTCCGGAGCCAGAGCTGAGGAAA 1380

DB 1321 TGTGTAACCTCATCATCGACCTCTCATTTATGCACTCCGGAGCCAAAGAGCTGAGGAAA 1380  
QY 1381 CCTTCAAGAGATCATCTGTTCTCTCCTCTGCTGGCTGGCTTGTGACTGTTCTAGCAGAT 1440  
DB 1381 CCTTCAAGAGATCATCTGTTCTCTCCTCTGCTGGCTGGCTTGTGACTGTTCTAGCAGAT 1440  
QY 1441 ACTAGCTGGGACAGAGGAAGTACTAAAAACATGACCAAGAGACTTCTTCATCTCCACAC 1500  
DB 1441 ACTAGCTGGGACAGAGGAAGTACTAAAAACATGACCAAGAGACTTCTTCATCTCCACAC 1500  
QY 1501 AACATGAATGCTGCTTGGACACAGCTGCTTCTTCTAGTATTAAGCAGAGGTGAGAA 1560  
DB 1501 AACATGAATGCTGCTTGGACACAGCTGCTTCTTCTAGTATTAAGCAGAGGTGAGAA 1560  
QY 1561 ATCTGCTGCACAAATTCACATTTATCATGTTTGTGATGCAAAAAAATGCCAGGCTC 1620  
DB 1561 ATCTGCTGCACAAATTCACATTTATGATGTTTGTGATGCAAAAAAATGCCAGGCTC 1620  
QY 1621 TGTACATGCTAATGCTGCTTCTTGGGCTGTCATTTGTAATTCATTCGACGCTG 1680  
DB 1621 TGTACATGCTAATGCTGCTTCTTGGGCTGTCATTTGTAATTCATTCGACGCTG 1680  
QY 1681 TAGACACTTTGAATTTCTAGAAAAAGAAAGCTTCCATTTAAAGCATATCAGTGTCT 1740  
DB 1681 TAGACACTTTGAATTTCTAGAAAAAGAAAGCTTCCATTTAAAGCATATCAGTGTCT 1740  
QY 1741 TGTATTCACGAGGATTTGGCACTTGTGCTTTAGGAAACATAGAAATCATAATCA 1800  
DB 1741 TGTATTCACGAGGATTTGGCACTTGTGCTTTAGGAAACATAGAAATCATAATCA 1800  
QY 1801 TTAACATGTCACCTGATAAAGTAACTTCTTATTTATATATATATATATATATATAT 1860  
DB 1801 TTAACATGTCACCTGATAAAGTAACTTCTTATATATATATATATATATATATAT 1860  
QY 1861 ATTTGAATGTCAGTGGGGTGGATATTTGAACATAGATCTTGGTCAATTAACAATC 1920  
DB 1861 ATTTGAATGTCAGTGGGGTGGATATTTGAACATAGATCTTGGTCAATTAACAATC 1920  
QY 1921 AACTCAAAATTTTAACTAAATAAAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1980  
DB 1921 AACTCAAAATTTTAACTAAATAAAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1980  
QY 1981 AAAAA 1985  
DB 1981 AAAAA 1985

RESULT 2

US-09-884-211a-1  
; Sequence 1, Application US/09884211a  
; Publication No. US20030032791A1  
; GENERAL INFORMATION:  
; APPLICANT: Alan et. al.  
; TITLE OF INVENTION: NOVEL MELANOCORTIN-4 RECEPTOR SEQUENCES AND  
; TITLE OF INVENTION: SCREENING ASSAYS TO IDENTIFY COMPOUNDS USEFUL  
; TITLE OF INVENTION: IN REGULATING ANIMAL APPETITE AND METABOLIC RATE  
; FILE REFERENCE: PC10743A  
; CURRENT APPLICATION NUMBER: US/09/884,211a  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: 60/213,909  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1708  
; TYPE: DNA  
; ORGANISM: Feline MC4R Nucleotide Sequence  
US-09-884-211a-1

Query Match 58.8%; Score 1166.6; DB 9; Length 1708;  
Best Local Similarity 83.5%; Pred. No. 1.8e-297;  
Matches 1418; Conservative 0; Mismatches 224; Indels 57; Gaps 6;



QY 14 GAGCAGCTGATGCGAACATGTGACGACGATTCAGCTCCTGGTGGCTCGCGGCAACTC 73  
DB 15 GAGCAGCTGATGCGAACATGTGACGACGATTCAGCTCCTGGTGGCTCGCGGCAACTC 74  
QY 64 GAGCAGCTGATGCGAACATGTGACGACGATTCAGCTCCTGGTGGCTCGCGGCAACTC 123  
DB 65 GAGCAGCTGATGCGAACATGTGACGACGATTCAGCTCCTGGTGGCTCGCGGCAACTC 124  
QY 74 GGAGAAATTAATTTTGAAGAACCTGACTGAATGCTCAGGCTAAAGTTAAGTTGAAGGGA 133  
DB 124 GGAGAAATTAATTTTGAAGAACCTGACTGAATGCTCAGGCTAAAGTTAAGTTGAAGGGA 183  
QY 134 GGAGAAATTAATTTTGAAGAACCTGACTGAATGCTCAGGCTAAAGTTAAGTTGAAGGGA 193  
DB 184 GGAGAAATTAATTTTGAAGAACCTGACTGAATGCTCAGGCTAAAGTTAAGTTGAAGGGA 201  
QY 194 CAGACTCTTTTGAATTAAGAAATGAGCAATTTTCAGAAATCGAAGATGTTACAGTGAAGTGTGAT 253  
DB 202 CAGACTCTTTTGAATTAAGAAATGAGCAATTTTCAGAAATCGAAGATGTTACAGTGAAGTGTGAT 261  
QY 254 CGAGCTGTACCTTGGAGACAGTAAGAGCTTCCACTGCCAGCTTTTGGAGCAGCGGACAG 313  
DB 262 CAGAGCGGTTTCTGGGAGACAGTAAGAACTTCCACTTTTCCAGCC--TGGGAGCAGCTGACAT 319  
QY 314 GTACTCAACACCTTGGCAGGCGCAGCTGGATCCTCAGAACTTTGGGACCGCAGGAGGGG 373  
DB 320 TTACTC-ACAACAGGATGCCAATTTTCAGCTCAGAACTTTTCGGGCGACAAAGGCGTGG 378  
QY 374 AGAATATCACCGGGGCTCCCTGGCTGGAGAGCGCGAATCAGTCCCGAGGGGCTGCGATA 433  
DB 379 AGAATATCACCGGGGCTCCCTGGCTGGAGAGCGCGAATCAGTCCCGAGGGGCTGCGATA 438  
QY 434 CACTGTGTGAGGATGAACCTTCCAGCTTCCAGCGGAAATGCACACTTCTTCCACTTCTG 493  
DB 439 CAC-TGGTGCAGGATGAACCTTCCAGCTTCCAGCGGAAATGCACACTTCTTCCACTTCTG 497  
QY 494 GAACCGCAGCCTTACGAGCAGCAGCGGACGCACTGAGTCCCTTGGGAAAGGCTACCC 553  
DB 498 GAACCGCAGCCTTACGAGCAGCAGCGGACGCACTGAGTCCCTTGGGAAAGGCTACCT 557  
QY 554 CGACGGGGATGCTACGAGCAACTTCTGCTCTCCCGGAGGTGTTCTGACTCTGCGGGT 613  
DB 558 TGATGGAGGTGTTATGAGCAACTTTTGTCTCCCTGAGGTGTTGTGACTCTGCGGTG 617  
QY 614 CATAAGCTTCTGAGAGCAATTTCTGGTATGCTGGCAATAGCCAAAGCAAGAAATTCGA 673  
DB 618 CACAGCTTCTGAGAGCAATTTCTGGTATGCTGGCAATAGCCAAAGCAAGAAATTCGA 677  
QY 674 CTCACCATGCTACTTTTCTATCTGAGCTGGCTGGCTGGCGATATGCTGTGAGCGTTT 733  
DB 678 TTGCGCCATGCTACTTTTCTATCTGAGCCTGGCTGGCTGGCTGATATGTTGTGAGCGTGT 737  
QY 734 CAACGGGTGACAGACCATCTCATCACCTTGTGAACAGTACGGATACGGACGCGCAGAG 793  
DB 738 AAACGGATCGAAACCATTTGTCATCACCTTATTAACAGTACAGATACGGACGCGCAGAG 797  
QY 794 TTTCAGGTGAATTAATGATATGCTATGCTGCGGTGATCTGAGCTTCTTCTGCTGCTC 853  
DB 798 TTTCAGGTGAATTAATGATATGCTATGCTGCGGTGATCTGAGCTTCTTCTGCTGCTC 857  
QY 854 GATTTCAGCTCTCTCAATTCAGTGGACGAGTACTTACTATCTTTTATGCCCTCCA 913  
DB 858 GATTTCAGCTCTCTCAATTCAGTGGACGAGTACTTACTATCTTTTATGCTCTCCA 917  
QY 914 GTACCATTAACATCATGAGGTGAGGGGTTGGATCATCATGATTGCTGCGGGG 973  
DB 918 GTACCATTAACATCATGAGGTGAGGGGTTGGATCATCATGATTGCTGCGGGG 977  
QY 974 TTGCAGGTGTACGGCATCTTTGTCATCAATTTACTCGGACAGTACTGCTGCTATCATCTG 1033  
DB 978 TTGCAGGTGTACGGCATCTTTGTCATCAATTTACTCGGACAGTACTGCTGCTATCATCTG 1037  
QY 1034 CTTATCATCAGCATGTTTCTTACCATGCTGGCCCTCATGGCTTCTCTTACCTCCACATGTT 1093  
DB 1038 CTTATCATCAGCATGTTTCTTACCATGCTGGCTCTCATGGCTCTCTCTATGCTCCACATGTT 1097

QY 1094 CCTCATGCCAGACTGCACATCAAGAGAATCGCGTCTCTCCCGGCGACCGGACCATCCG 1153  
DB 1098 CCTCATGCCAGACTGCACATTAAGAGAATTCGTCTCTCCCGGCGACTGSCACCATCCG 1157  
QY 1154 CCAAGGGGCGCAACATGAAGGGTGCCATTACCTTGACCATCTCATTTGGGGTCTTTCGTCGT 1213  
DB 1158 CCAAGGGGCGCAACATGAAGGGTGCAATTAACCTGACCATCTGATTGGGGTCTTTCGTCGT 1217  
QY 1214 CTGCTGGGCTCCACTTCTCTCCACTTGTATATCTACATCTTGTGCCCCAGAAATCCATA 1273  
DB 1218 CTGCTGGGCGCCGCTTCTCTCCACTTAATATCTACATCTTGTGCCCCAGAAATCCATA 1277  
QY 1274 CTGCTGGTGTCTCATGCTCTCACTTTAACTTTGTACCTCATCTGTATCTGTAATCCAT 1333  
DB 1278 CTGCTGGTGTCTCATGCTCTCACTTTAACTTTGTATCTCATCTGTAATTCAT 1337  
QY 1334 CATCGACCTCTCATTTATGCACCTCCGAGGCGCAAGCTGAGGAAACCTTCAAGAGAT 1393  
DB 1338 CATCGACCTCTCAATTTATGCACCTCCGAGGCGCAAGAACTAAGGAAACCTTCAAGAGAT 1397  
QY 1394 CATCTGTTGTATCTCTCTGGTGGCTTTGTGACTTTGTAGCAGATACTAGCTGGGAC 1453  
DB 1398 CATCTGTTGTATCTCTCTAGGCGCTCTGTGATTTGTCTAGCAGATACTAATCTGTCAG 1457  
QY 1454 AGAGGAAGTACTAAAAACATGCACAGAGACTTCTTCATCTCACAAACATGAATCTGTG 1513  
DB 1458 A-----TAGAAGCTGCATAAGAGACTTCTTCATCTTACAGACCGGAACATTG 1507  
QY 1514 TGCTTGGACAAACAGCTCTCTTCAGTATAGGAGGAGTTGAGAAATCTGTTGTCACAA 1573  
DB 1508 TGCTTGTATGACCTTTCTCTCTGTGTAAGGCACTGGGTGAGACTATCTGTTGTATAA 1567  
QY 1574 ATTCAACTTTATGATGTTTGTGATCTGAAAAAATAATGCCAGGCTCTGTACATGCTAA 1633  
DB 1568 ATTAAAGTTTCATGACTTTTGTGGAATGGAACAATGCCAGTCTCTGTACATTTCTAA 1627  
QY 1634 TGTCATCTACTTTTGGGCTGTGCTATGTTAAATCCAT--TTGACGCGTGTAGACACTTTGA 1692  
DB 1628 TGCTTCTACTACTTTTGGCTGTACAATGTTAATCCATATATAGTTGTAGGACATATGA 1687  
QY 1693 ATTTCTAGAAAAAGAAAAA 1711  
DB 1688 ATGTATAAAAAAATAAAAAA 1706

RESULT 3  
US-09-910-180-1  
; Sequence 1, Application US/09910180  
; Publication No. US20030082678A1  
; GENERAL INFORMATION:  
; APPLICANT: Hsiung, Hansen  
; APPLICANT: Smith, Dennis  
; APPLICANT: Zhang, Xing-yue  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING BODY WEIGHT IN BOVINE  
; FILE REFERENCE: P-12621  
; CURRENT APPLICATION NUMBER: US/09/910.180  
; CURRENT FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1950  
; TYPE: DNA  
; ORGANISM: Bovine  
US-09-910-180-1

Query Match 48.8%; Score 968.6; DB 9; Length 1950;  
Best Local Similarity 76.4%; Pred. No. 3.9e-245;  
Matches 1328; Conservative 0; Mismatches 379; Indels 32; Gaps 10;  
QY 224 AGAATCGAAGATGTTACAGTGAAGGTGATCGGAGCTGTACCTGGAGACAGATGAAGACT 283  
DB 68 AGCAGCCTAAGATTTTCAAGTGTGCTGACAGAGCCACACTTGAAGAGACTGAAAACT 127

QY 284 CCNCTGCCAGCCTTTTGGAGCAGGGGACAGAGGTACTCAACACCTGGCAGGCGCAGCTGGATC 343  
Db 128 TCTTTTCCAGC--TCCGGAGCATGGGACATTTATTC-ACAGGAGGCATCCACTCTCCGC 184  
QY 344 CTCAGAACTTTGGGAGC---CACGGAGAGGGGAGAACATCACCCGGGCTCCCTGGCTG 399  
Db 185 CGCCTAACCTTTTGGTGGGCAAGTCAAGACTGGAGAAAGGTGCTGAGGCTGCCAGATCC 244  
QY 400 GAGAGCGGAATCAGTCCCGAGGGGTCTGCATACACTTTGTCAGAGATGAATCCACOC 459  
Db 245 AGGAGGTCAGTCAGTCAGTCAGAGGGGACCTGAATCCAAA-----ATGAACCTTACCC 295  
QY 460 TTCAGACAGGAATGCACACTTCTCCACTTCTGGAACCGCAGCAGCTACGAGCAGCAG 519  
Db 296 AGCCCCCTTTGGGATGCACACTCTCTCCACTCTGGAACCGCAGCAGCAGCAGCAGC 355  
QY 520 GAAAGCCCACTCAGTCCCTTGGCAAGGCTACCCGAGGGGATCTACGAGCACTCT 579  
Db 356 CCATGTCTAGTGAGTCCCTGGCAAGGCTACTCGGACGGGGGTGCTATGAGCAGCTCT 415  
QY 580 TCGTCTCCCGGAGGTGTTCGTGACTCTGGGGTCTAAGCTTTGCTGGAGAACATTTCTGG 639  
Db 416 TTGTCTCTCCGAGGTGTTGTGACTCTGGGGTCTACAGCTTGTGGAGATATTCGG 475  
QY 640 TGATCGTGCAATAGCCAAAGAACAGAAATCTGCACCTCACCCATGTACTTTTCACTGTA 699  
Db 476 TGATCGTGCCCATGCCAAGAACAGAAATCTGCACCTCACCCATGTACTTTTCACTGCA 535  
QY 700 GCCTGGCTCTGCCGATATGCTGGTGAGGGTTTCAACGGGTCAGAGACCATCGTCATCA 759  
Db 536 GCCTGGCTGGCTGACATGTTGGTGAGGGTTTCAACGGGTCGGAACCATTTGTCATCA 595  
QY 760 CCCTGTTGAACAGTACGGATACGGACGGCGCAGAGTTTTCACGGTGAATTTGATAATGCA 819  
Db 596 CCCTGCTGAACAGCAGGACGGACGGCGCAGAGCTTCACGGTGGATATTGACAATGCA 655  
QY 820 TTGACTCGGTATCTGTAGCTCCTTGTCTGCCTCGATTTGCAAGCTGCTCTCAATTGCGAG 879  
Db 656 TTGACTCGGTGATCTGTAGCTCCTTGTCTGCCTCGATTTGCAAGCTGCTCTCAATTGCGAG 715  
QY 880 TGGACAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATAACATCATGACGGTGAGGC 939  
Db 716 TGGACAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATAACATCATGACGGTGAGGC 775  
QY 940 GGGTTGGGATCATCATAGTTGCAATCTGGCGGGCTTGCACGGTGTGACGATCTTTGTTCA 999  
Db 776 GGGTGGCGATCACCATCAGCGCATCTGGCGAGCCTGCACGGTGTGCGGGCTCTGTTCA 835  
QY 1000 TCATTTACTCGACAGTACTGCTGTCTCATCATCTGCTCATCACCATGTTCTTCACCATGC 1059  
Db 836 TCATTTACTCGACAGCAGTGTCTGTATCATCTGCTCATCACCATGTTCTTCACCATGC 895  
QY 1060 TGGCCCTCATGCTTCTCTACGTCCACATGTTCTCATGCGCAGACTGCACATCAAGA 1119  
Db 896 TGGCTCTCATGGCTCTCTATGTCCACATGTTCTCATGCGCAGACTGCACATCAAGA 955  
QY 1120 GAATCGCGGTCTCTCCGGCACCGCACCATCCGCCAAGGGGCCAACATGAAGGTGGCA 1179  
Db 956 GGATCGCGGTCTCGCCAGTAGCGGCACCATCCGCCAGGGCCCAACATGAAGGGGGCA 1015  
QY 1180 TTACCTTGACCAATCATTTGGGGTCTTTCGGTCTGCTGGGCTCCATCTTCCTCCACT 1239  
Db 1016 TTACCTTGACCAATCATTTGGGGTCTTTCGGTCTGCTGGGCTCCATCTTCCTCCACT 1075  
QY 1240 TGATATTTACATCTCTTGTCCCAAGATTCATCTGTGTCTCATGTCTCACTTCA 1299  
Db 1076 TGATATTTACATCTCTTGTCCCAAGATTCATCTGTGTCTCATGTCTCACTTCA 1135  
QY 1300 ACTTGTACCTCATCTGTATGTAATCTCATCATCGACCTCTCATTTATGACACTCC 1359  
Db 1136 ACCTGTACCTCATCTGTATGTAATCTCATCATCGACCTCTCATTTATGACCTCC 1195  
QY 1360 GGAGCCAAAGCTGAGGAAAACCTTCAAAGAGATCATCTGTTGCTATCCTCTGGGTGCC 1419

Db 1196 GGAGCCAAAGAACTGAGGAAACCTTCAAAGAGATCATTTTGTCTCTCTCTAGGTGGCC 1255  
QY 1420 TTTGTGACTTGTCTAGCAGATACTAGCTGGGACAGAGGAAGTACTTAAACACATGCACCA 1479  
Db 1256 TCTGTGATTTGTCTAGCAGATATTAATGGGACAAACCCGATGCTTAAACACAAAGCTTAA 1315  
QY 1480 GAGACTTCTTCATCCTCA---CACAAACATGAACCTGTGTCTTGGACAAACAGCTGCTTCT 1535  
Db 1316 GAGACTTCTCTCTCATATCTACAACCTGAACAGTCTGTATCAGCCACAGCTTTTCT 1375  
QY 1536 TCAGTATAAGCGAGGTGAGAAATATCTGTGACAAATCAACTTTATGATGTTTGA 1595  
Db 1376 TCTGTGAGGCGATGGAGTGAATAATTTCTATTGTATCAGTTGAAGTTTGTGATTTTTTC 1435  
QY 1596 TCTGAAAATAAATGCCCAGGCTCTGTACATTTGCTAATGCTATGCTACTCTTGGCTGT 1655  
Db 1436 TGATGTGAACAG-TGCCAGCTCTGGGTATTTAATGTCTACTCTTCTGGCTGT 1494  
QY 1656 GCATTGTAAATCCATTTTC-GACGCTGTAGACACTTTTGAATTTCTAGAAAA-----GAAAA 1709  
Db 1495 AAAATGTGAATCCACATCACAGGTTATAGGCACATGCAATTTATAAAAAAGAGAATAA 1554  
QY 1710 AAGCTTCCATTAAGACATATCAGTGT----TTCCTGTTTATTCAGAGATTTGGCATT 1765  
Db 1555 AAGTCTTATGAGGAGTTTAACAGTGTTCCTTCTTGTATTATTAAGAGATGTGACATT 1614  
QY 1766 TCGTTGCTTTAGGAACATAGAAATCATAGATCATTAACATATGATAGCTGATAAGTAAC 1825  
Db 1615 TCGTTGCTTT-TGTAACTGGAATCAACAGCTTCAATAGTATATCTCTCATAGTGT 1673  
QY 1826 TTTTATATATATATATATATACATGAAATGTGCAGATTTGAATGTAGCATGGGGTGA 1885  
Db 1674 TTTTATGTTATACTTTTACAACACTGAAGTGTAAAAATTTGATTTCTAGCATTTAGGGGAGA 1733  
QY 1886 TATTGACAAATAGATACTTGTGTCATTAACAAATCAACTGAATTTTAAAGTAAATAAT 1944  
Db 1734 AATATTGAGACATATTGCTTAATCATAAAAAAGCTGAAATTTACAGTAAATTAAT 1792

## RESULT 4

US-10-288-160-15

; Sequence 15, Application US/10288160

; Publication No. US20030105024A1

; GENERAL INFORMATION:

; APPLICANT: Cone, Roger D

; Fan, Wei

; Boston, Bruce A

; Kesterton, Robert A

; Lu, Dongsu

; Chen, Wenbiao

; TITLE OF INVENTION: Methods and Reagents for Discovering and

; Using Mammalian Melanocortin Receptor Agonists and Antag

; To Modulate Feeding Behavior in Animals

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert &amp; Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/288,160

; FILING DATE: 05-NO. US20030105024A1-2002

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/706,281





FILING DATE: 21-AUG-92  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/92  
FILING DATE: 10-SEP-92  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0528/93  
FILING DATE: 05-MAY-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimballa, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1102.0160000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1650 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (cDNA)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 616..1590  
US-10-052-545-15

Query Match 21.4%; Score 424.8; DB 12; Length 1650;  
Best Local Similarity 69.2%; Pred. No. 1.5e-101; Indels 3; Gaps 1;  
Matches 595; Conservative 0; Mismatches 262; Indels 3; Gaps 1;  
QY 590 GGAGGTGTTGCTGACTGCGGGTGCATAGCTTCTGGAGAACATCTCTGGTATCGTGGC 649  
DB 735 GGAGGTGTTTCTCACTCTGGTGTCTATCAGCCCTTTGGAGAACATCTCTGGTATCGTGGC 794  
QY 650 AATAGCCAGAACAAATCTGCATCACCATGACTTCTTTTCTATCTGTAGCCCTGGTGT 709  
DB 795 CATAGTGAAGAACAAAACCTGCATCCCTCCCTGTTCTTCTGTCAGCGTGGCAGT 854  
QY 710 GCGCGATATGCTGGTGGGCTTCCAAACGGTCCAGAGACCATCGTATCATCCCTGTGAA 769  
DB 855 GCGGACATGCTGGTGGAGATGTCAGTGCCTGGGAGACCATCACCATCTACCTACTCAA 914  
QY 770 CAGTACGGA---TACGGAGCGCGAGAGTTTACGGTGAATATTGATAATGTTCACTGACTC 826  
DB 915 CAACAAGCACCTAGTGATAGACAGACGCTTTTGGCGCCACATGTGCAATGTTGACTC 974  
QY 827 GTGATCTGTAGTCTCTGCTGCGCTGCAATTCAGCGCTGCTCTCAATTCAGATGGACAG 886  
DB 975 CATGATCTGCATTTCCGTGGTGGCATCCATGTGACGCTTACTGGCCATTTGCACTGGATAG 1034  
QY 887 GTACTTTACTATCTTTTATGCCCCCTCCAGTACCATACATCATCAGCGTGAGCGGGTTGG 946  
DB 1035 GTAGTTCACCACTTCTACGCCCTGGCTACCCACCATCATGACCGGAGGCGGCTCAGG 1094  
QY 947 GATCATCATAGTTGATCTGGCGGCTTGCAGCGGTGCAGGATCTTGTTCATCATTTA 1006  
DB 1095 GGCCATCATCGCGCGCATCTGGGCTTCTGCACGGGCTGGCGCATTTGCTTCATCTCTGA 1154  
QY 1007 CTCGGACAGTACTGCTGTATCATCTGCTCATCAGCATGTTCTTCAACATGTCGCCCT 1066  
DB 1155 CTGAGATCCACCTAGCTATCTGCTGCTCATCTGCTCATCTGCTTCTGCTATGTTCTCT 1214  
QY 1067 CATGGCTTCTCTACGTCCACATGTTCTCATGGCCAGACTGCATCATCAAGAGATCGC 1126  
DB 1215 CTGTTGTCTCTGTACATACATGTTCTCTTGGCGGAGCTCAGCTCAAGCGGATCGC 1274  
QY 1127 CGTCTCCCGGGCAGCGCACCATCCGCAAGGGGCCAACATGAAGGGGTGCCATTACCTT 1186  
DB 1275 GCTCTCGCGGGGCCAGCTCTGCGCGCAGAGACCATGAGCATGGCAGGGCGGCTACCGT 1334  
QY 1187 GACCATCATCTATGGGGTCTTGTGCTGCTGCTGGGTCCATGTTCTCTCCACTGTATAT 1246  
DB 1335 CACCATGCTGCTGGGGTGTGTTACCGTGTGCTGGGCCCCGTTCTTCTTCTCATCTCACTTT 1394

QY 1247 CTACATCTCTGTCCCGAGAATCCATACTGTTGTGCTTCATGTCTCACCTTAACTTGA 1306  
DB 1395 AATGCTTTCTTGGCCCTCAGAACCTTACTCTCGCTTCATGTCTCACCTTCAATATGA 1454  
QY 1307 CCTCATCTGATCATGTGTAATCCATCATCGACCCCTCTCATTTATGACATCCGGAGCCA 1366  
DB 1455 CCTCATACTCATCATGTGTAATCCGTGATGGACCCCTCTCATATATGCTTCCGAGCCA 1514  
QY 1367 AGAGCTGAGGAAAACCTTCAAGAGATCATCTGTTGCTATCTCTGGTGGCCCTTTTGA 1426  
DB 1515 AGAGATGCGGAGAACCTTTAAGGAGATATTTCCTGCCGTTTTCAGATCGCCTGAG 1574  
QY 1427 CTTGCTTAGCAGATACTAGC 1446  
DB 1575 CTTTCCAGAGAGGATTAAC 1594

## RESULT 7

US-09-903-395-1  
Sequence 1, Application US/09903395  
Patent No. US20020068324A1  
GENERAL INFORMATION:  
APPLICANT: Allen, Keith D.  
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING  
FILE REFERENCE: R-653  
CURRENT APPLICATION NUMBER: US/09/903,395  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/218,074  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/243,958  
PRIOR FILING DATE: 2000-10-26  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1675  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-903-395-1

Query Match 20.5%; Score 406.6; DB 10; Length 1675;  
Best Local Similarity 67.7%; Pred. No. 9.9e-97;  
Matches 603; Conservative 0; Mismatches 279; Indels 9; Gaps 2;

QY 523 ACCGCACTGAGTCCCTTGGCAAGGCTACCCGACGGGGGATGCTACGAGCAACTCTTCG 582  
DB 168 ACCCTGACGCCCCCTCTGCCAGCAACCGGAGCGGAGTGGGTCTTGTGACGAGGTCTTCA 227  
QY 583 TCTCCCGGAGGTGTTCTGACTCTGGGGTCTAAGCTTCTGGGAGAACATCTCTGTTGA 642  
DB 228 TCAAGCGGAGGTCTTCTCGGCTCTGGGCACTGCTGATGGAAGAACATCTCTGTTGA 287  
QY 643 TCGTGGCAATPAGCAAGAACAAATCTGCACCTCACCCATGATCTATTTTTCATCTGTAGCC 702  
DB 288 TCCTGGCTGTGGTGGAGAACTGCAACCTGCACTTCCCATGTACTTCTTCTGTCGACGC 347  
QY 703 TGGCTGTGGCGGATATGCTGGTGGAGCGTTTCCAAACGGGTCAGAGACCATGTCATCACCC 762  
DB 348 TGGCTGACGCGGACATGCTGGTGGAGCCTGTCCAACCTCCCTGGAGACCATCATGATCCCG 407  
QY 763 TGTGTAACAG---TAGGATACGAGCGCAGAGTTTTCACGGTGAATATTGATAATGTCA 819  
DB 408 TGATCAACAGCGACTCCCTGACCTTGGAGGACCATGTTATTCACGACATGGATAATCT 467  
QY 820 TTGACTCGGTGATCTGTAGTCTCTTGTCTGCTCGCTCGATTTTTCAGCGCTCTCTCAATTGAG 879  
DB 468 TCGACTCTATGATTGATCTCTCCCTGGTGGCCCTCCATCTGCAACCTCTTGGCCATGCCA 527  
QY 880 TGGACAGGTACTTTTACTATCTTTTATGCGCTCCAGTACCATACATCATGACGTTGAGGC 939  
DB 528 TCGACAGGTAGCTCAGCATCTTCTATGCCCCCTGGTACCACAGCATCATGACAGTTAGGA 587

940	QY	GGGTTGGGATCATCATCAGTTGCTATCGGGGGGTTGCACGGTGTACAGGATCTTGTTCA	999
588	Db	AAGCCCTCACCCTTGATCGGGGTCTATGGGTCTGCTGCGCATCTGCGGGCTGATGTTCA	647
1000	QY	TCATTTACTCGGACAGTACTGCTGTATCATCTGCGCTCATCACATGTTCTTCCACATGC	1059
648	Db	TCATCTACTCCGAGACGAAGATGGTCATCGTGTGTCTCATCACCATGTTCTTGCCATGG	707
1060	QY	TGGCCCTCARGGCTTCTCTAGCTCCACATGTTCTCATGTCGACACTGCACATCAAGA	1119
708	Db	TGCTCTCTCATGCGGCACCCATATATCCACATGTTCTCTTTCGCGAGGCTCCAGTCCAGC	767
1120	QY	GAATCGCGCTCTCC-----CGGGCACCGGCACCATCGGCCAAGGGGGCAACATGAGG	1173
768	Db	GCATCGAGTGCTGCCCCCTGCTGGGGTGTGGCCCCACAGCAGCACTTCTGTGATGAAGG	827
1174	QY	GTCCATTACTCTTGACCATACTCATTTGGGTCTTCTGCTGCTGCTGGGTGCCATTTCTTCC	1233
828	Db	GGGCTGTCAACCATCACTATCCTGCTGGTGTTTTTCATCTTCTGCTGGGCGCTTCTTCC	887
1234	QY	TCCACTTGATATTCTACATCTCTTGTCGCCAGAAATCCATACTGTGTGTGCTTCATGTCTC	1293
888	Db	TCCACCTGGTCTTCATCATCACTGCCCCACCAATCCCTACTGCATCTGCTACACGGCCC	947
1294	QY	ACTTTAACTGTACCTCATCTCATATGTGTAACTCCATCATCTGACCCCTCTCATTTATG	1353
948	Db	ATTTCAACACTTACCTGGTCTCATCATGTGCAACTCCGCTCATCGACCCCTCATCTACG	1007
1354	QY	CATCTCGGAGCCAAAGAGCTGAGGAAACCTTCAAGAGATCATCTGTGTCT	1404
1008	Db	CTCTCGGAGCCTTGGAGCTCGCAACACGCTTCAAGGAGATTTCTCTCGGGCT	1058

## RESULT 8

US-10-288-160-11  
: Sequence 11, Application US/10288160  
: Publication No. US20030105024A1  
: GENERAL INFORMATION:  
: APPLICANT: Cone, Roger D  
: Fan, Wei  
: Boston, Bruce A  
: Kesterton, Robert A  
: Lu, Dongsu  
: Chen, Wenhao  
: TITLE OF INVENTION: Methods and Reagents for Discovering and  
: Using Mammalian Melanocortin Receptor Agonists and Antagonists  
: To Modulate Feeding Behavior in Animals  
: NUMBER OF SEQUENCES: 19  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
: STREET: 300 South Wacker Drive  
: CITY: Chicago  
: STATE: IL  
: COUNTRY: USA  
: ZIP: 60606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/10/288,160  
: FILING DATE: 05-No. US20030105024A1-2002  
: CLASSIFICATION: <Unknown>  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/706,281  
: FILING DATE: 04-SEP-1996  
: ATTORNEY/AGENT INFORMATION:  
: NAME: NO. US20030105024A1nan, Kevin E  
: REGISTRATION NUMBER: 35,303  
: REFERENCE/DOCKET NUMBER: 96,886  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 312-913-0001







;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/706,281  
;; FILING DATE: 04-SEP-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. US20030105024Alnan, Kevin E  
;; REGISTRATION NUMBER: 35,303  
;; REFERENCE/DOCKET NUMBER: 96,886  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312-913-0001  
;; TELEFAX: 312-913-0002  
;; TELEX: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1260 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA to mRNA  
;; FEATURE:  
;; NAME/KEY: 5'UTR  
;; LOCATION: 1..14  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 15..959  
;; FEATURE:  
;; NAME/KEY: 3'UTR  
;; LOCATION: 960..1260  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-288-160-3

Query Match 14.1%; Score 279; DB 9; Length 1260;  
Best Local Similarity 59.3%; Pred. No. 4.1e-63;  
Matches 512; Conservative 0; Mismatches 345; Indels 6; Gaps 2;

QY 548 CTACCCGACGGGGATGCTACAGCAACTCTTCCTCCCGAGGTGTCTGACTCT 607  
DB 92 CAACAGCTAGACGCTTGGTGCCTATGTGTCCATCCAGATGGCCCTCTCC 151  
QY 608 GGGGGTCATAAGCTTGTCTGAGAACATCTGTGATGCTGGCAATAGCAAG 667  
DB 152 AGGCTGGTGAAGTCTGGTGGAGATGTCTGGTGTATAGCCATACCAAAAC 211  
QY 668 TCTGCACTACCCATGACTTTTTCATCTGTAGCCTGGCTGTGGCCGATAT 727  
DB 212 CCTGCACTCGCCATGATTACTTCTGCTGGCCCTGTCTGACCTGATGTA 271  
QY 728 CGTTTCCAGCGGTGACAGACATCGTCACCCCTGTTGAA---CAGTACG 784  
DB 272 TGTACGATCGTGTGGAGACTACTATCTCTGCTGGAGTGGGCATCTCTG 331  
QY 785 CGCGCAGAGTTTCACGGTGAATATGTATATGTCATGCTGCTGATCTGACT 844  
DB 332 CAGAGTGGCTTGGTCAGCAGCTGGACAACCTCAITGACGTGCTCATCTGT 391  
QY 845 GCTCGCTCGATTTCAGCCTGCTCTCAATTCAGTGGACAGGTGACTTTACT 904  
DB 392 GGTGTCAGTCTCTGCTTCTGGCATCATGTGTATAGCCGCTACATCTCTA 451  
QY 905 TGGCTTCCAGTACCATTAACATCATAGCGGTGAGCGGGTTGGATCATCATG 964  
DB 452 TGGCTGCGTATACAGCATCTGAGCTGCGCCAGACGACGCGGCTGCTGG 511  
QY 965 CTGGGGGCTTGCACGGTGTGACGATCTGTGTCATCATTTACTCGGACAGT 1024  
DB 512 CTGGATGGTCAGCATCGTCTCCAGCACCCCTTTTATCACTACTACAAGCA 571  
QY 1025 CATCATCTGCTCATCACCATGTTCTTCAACATGCTGGCCCTCATGGCTT 1084  
DB 572 TCTGCTCTGCTGCTACITCTTCTTAGCCATGCTGGCACTCATGGCGATT 631  
QY 1085 CCACATGTTCTCATGGCCAGACTGCACATCAAGAGAATCGCC---GTCTCC 1141  
DB 632 CCACATGTTTCACGAGCGGTGCCAGCAGCTCCAGGGCATTTGCCAGCTCC 691

QY 1142 CGCACCATCGCCCAAGGGCCCAACATGAAGGTGCCATTACCTTGACCATCAT 1201  
DB 692 GCGGTCCATCGCCCAAGGCTTCTGCTCAAGGGTGTGCCACCCCTTACTATC 751  
QY 1202 GGTCTTCTGCTGTCTGCTGGGCTCCATCTCTCCCTCCACTTGATATCTAC 1261  
DB 752 GATTTTCTTCTGCTGTCTGGGCCCCCTTCTCTCTGCATCTCTTGTCTCAT 811  
QY 1262 CCAGAATCCATACGTGTGTGCTTCACTTTAACTTGTACCTCATCTCTGAT 1321  
DB 812 TCAGACCCCACTGCGAGCTGCATCTTCAAGAACTTCAACCTCTTCTCTCC 871  
QY 1322 GTGTAATCTCCATCATCGACCCCTCTCATTTATTCCTCGGCAAGAGCTG 1381  
DB 872 CCTCAGCTCCACTGTTGACCCCTCACTATGCTTTCGCGAGCCAGGAGCT 931  
QY 1382 CTTCAAAGAGATCATCTGTTGCT 1404  
DB 932 ACTCAAGGAGGTGCTGCTGCT 954  
RESULT 12  
US-09-815-944-19  
; Sequence 19, Application US/09815944;  
; Patent No. US20020038467A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Keith D.  
; APPLICANT: Matthews, William  
; APPLICANT: Moore, Mark  
; APPLICANT: Phillips, Russell  
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MELANOCYTE  
; TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS  
; FILE REFERENCE: R-654  
; CURRENT APPLICATION NUMBER: US/09/815,944  
; CURRENT FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 60/191,236  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: US 60/215,214  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,075  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/219,167  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 1260  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-815-944-19  
Query Match 14.1%; Score 279; DB 10; Length 1260;  
Best Local Similarity 59.3%; Pred. No. 4.1e-63;  
Matches 512; Conservative 0; Mismatches 345; Indels 6; Gaps 2;  
QY 548 CTACCCGACGGGGATGCTACAGCAACTCTTCCTCCCGAGGTGTCTGACTCT 607  
DB 92 CAACAGCTAGACGCTTGGTGCCTATGTGTCCATCCAGATGGCCCTCTTCT 151  
QY 608 GGGGGTCATAAGCTTGTCTGAGAACATCTGTGATGCTGGCAATAGCAAGAA 667  
DB 152 AGGCTGGTGAAGTCTGGTGGAGATGTCTGGTGTATAGCCATACCAAAACCG 211  
QY 668 TCTGCACTACCCATGACTTTTTCATCTGTAGCCTGGCTGTGGCCGATATG 727  
DB 212 CCTGCACTCGCCATGATTACTTCTGCTGGCCCTGTCTGACCTGATGTAAG 271  
QY 728 CGTTTCCAGCGGTGACAGACATCGTCACCCCTGTTGAA---CAGTACGGAT 784  
DB 272 TGTACGATCGTGTGGAGACTACTATCTCTGCTGGAGTGGGCATCTCTG 331  
QY 785 CGCGCAGAGTTTCACGGTGAATATGTATATGTCATGCTGCTGATCTGACTCT 844

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Db 332 CAGAGTGGCTTTGGTCAGCAGCTGGACACCTCATTTGACGCTCTCATCTGTGGCTCCAT 391
QY 845 GCTCGCTCGATTTGTCAGCTGCTCTCAATTTGAGTGGACAGGTACTTTTACTATCTTTTA 904
Db 392 GGTGTCCAGTCTCTGCTTCTCGGGCATCATGTATAGACCGGTACATCTCCATCTCTA 451
QY 905 TGCCCTCCAGTACCATAAACATCATGACGGTGGAGCGGTTGGGATCATCATCATAGTGCAT 964
Db 452 TGGCTGCGTTATACAGCATCTGACGCTGCCAGCAGCAGCGGCTGTCTGGGCAT 511
QY 965 CTGGGCGGCTTGCACGGTTCAGGCATCTGTTTCATCATTTACTCGGACAGTACTGCTGT 1024
Db 512 CTGGATGGTCAGCATGCTTCCAGCACCTCTTTATCACCTACTACAAGCACACAGCGGT 571
QY 1025 CATCATCTGCCTCATCACCATGTTCTTCCACATGCTGGCCTCATGCTTCTCTACGT 1084
Db 572 TCTGCTCTGCTGCTCACTTCTTCTAGCCATGCTGGCAGCTCATGGCATCTGTATGC 631
QY 1085 CCACATGTTCCATGCGCAGACTGCACATCAAGAAATCGCC--GTCTCCCGGGCAC 1141
Db 632 CCACATGTTTCAGAGAGTGGCAGCAGCTCCAGGGCATTTGCCAGCTCCACAAAAGCG 691
QY 1142 CGGCACCATCCGCAAGGGCCACATGAAGGTGCCATTTACTTGACCATCTCATTTGG 1201
Db 692 GCGGTCCATCCGCAAGGTTTGTGCTCAAGGTTGCTGCCACCTTACTATCTTCTGGG 751
QY 1202 GGTCTTCTGCTGCTGGGCTCCATTTCTTCCACTTGTATTTACATCTTCTTGTCC 1261
Db 752 GATTTCTTCTGCTGGGCGCCCTTCTCTGCTATCTCTGCTCATCTGCTCTGCCC 811
QY 1262 CCAGAAATCATCTGCTGCTGCTCATGCTCTCACTTTAACTTGATCTCTCATCTGATCAT 1321
Db 812 TCAGACCCCACTGCTGAGCTGATCTTCAAGAACTTCAACCTTCTCTCTCTCATCTGT 871
QY 1322 GTGTAACCTCATCTGACCTCTCATTTATGCACCTCCGAGCCAGACCTGAGGAAC 1381
Db 872 CTTCAAGAGATCATCTGTTGCT 1404
QY 1382 CTTCAAGAGATCATCTGTTGCT 1404
Db 932 ACTCAAGAGGTGCTGCTGTCT 954
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RESULT 13

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US-10-151-431-3
; Sequence 3, Application US/10151431
; Publication No. US20030044973A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Mountjoy, Kathleen G
; TITLE OF INVENTION: Mammalian Adrenocorticotrophic Hormone
; Receptors and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Allegrretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/151,431
; FILING DATE: 20-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,298
; FILING DATE: <Unknown>
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; APPLICATION NUMBER: US 07/866,560
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030044973Alban, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2012 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 694..1587
; OTHER INFORMATION: /product= "Human
; adrenocorticotrophic hormone receptor"
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..693
; NAME/KEY: 3'UTR
; LOCATION: 1588..2012
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-151-431-3
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Query Match 13.9%; Score 275.4; DB 9; Length 2012;
Best Local Similarity 60.8%; Pred. No. 5.1e-62;
Matches 497; Conservative 0; Mismatches 296; Indels 24; Gaps 2;

QY 590 GGAGGTGTTCTGAGTCTCTGGGGTCTAATAAGCTTGTGGAGAACATTTCTGGTGTGCTGGC 649
Db 777 GGAGATATATTTTACAAATTTTCCATTTGTGGAGTTTGGAGAAATCTGATCGTCTGCTGGC 836
QY 650 AATAGCAAGAACAAGAAATCTGCACCTACCCCATGTACTTTTTCATCTGTAGCCTGGCTGT 709
Db 837 TGTGTTCAAGAATAAGAATCTCCAGGCACCCATGTACTTTTTCATCTGTAGCTTGCCCAT 896
QY 710 GGCCGATATCTGTTGAGCGTTTCCAAAGGGTTCAGAGACATCGTCTCATCACCCTGTTGAA 769
Db 897 ATCTGATATGCTGGCAGCCTATATAAGATCTTGGAAATAATCTCTCATCATATTGAGAA 956
QY 770 CAGTACGGATACGGACGGC---AGAGTTTCAGGGTGAATATGTGTAATGTCTATTTGACTC 826
Db 957 CATGGGCTATCTCAAGCCACGTGGCAGTTTGAACACACAGCGGATGACATCATCGACTC 1016
QY 827 GGTGATCTCTAGTCTCTGCTCGCCCTCGATTTGACGCTGCTCTCAATTGCACTGGACAG 886
Db 1017 CCGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1076
QY 887 GTACTTTACTATCTTTTATGCGCTCCAGTACCATCAATCATCATGACGGTGGAGCGGTTGG 946
Db 1077 CTACATCACCATCTTCCAGCAGCTGGGTACACAGACCTGTCGACCATCGCGGCACTGT 1136
QY 947 GATCATCATCTGATCTGGGCGGCTTGGACGGTGTGACGGTGTGAGGATCTTGTTCATCATTTA 1006
Db 1137 GGTGGTGTCTTACGGTCATCTGGACGTTCTGACGGGGACTGGCATCACCATGCTGTATCTT 1196
QY 1007 CTCGGACAGTACTGCTGTCTCATCTGCTCATCACCATGCTCTTCCACCATGCTGCGCCT 1066
Db 1197 CTCCTCATCTGTCGACAGTACCTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1256
QY 1067 CATGGCTTCTCTACGTCACATGTTCTCTATGCGCAGACTGCACATCAAGAGAAATCGC 1126
Db 1257 CATCTGTGCTCTATGTGCACATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
QY 1127 CGTCTCTCCGGGACCGGACCATCCGCAAGGGGCAACATCGGCAAGGGGTGCCATTTACCTT 1186
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